

ME

177157

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From: Chernyshev, Olga
Sent: Friday, January 20, 2006 1:18 PM
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Subject: 09/612,921, sequence search request

Please search SEQ ID NO: 3 down to 95% identity and also 30 contigs of SEQ ID NO: 3 in regular and pending databases.
Thank you very much!

Olga N. Chernyshev, Ph.D.
AU 1649
REM 3C89
2-0870
mail 4C70

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Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
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Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.6
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OW nucleic - nucleic search, using sw model

Run on: January 27, 2006, 18:52:33 ; Search time 3013 Seconds
(without alignment)
8829.318 Million cell updates/sec

Title: US-09-612-921B-3

Perfect score: 468

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 300 summaries

Database :

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3: gb_env:*
4: gb_env:*
5: gb_ov:*
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7: gb_pat:*
8: gb_ph:*
9: gb_pr:*
10: gb_ro:*
11: gb_ro:*
12: gb_un:*
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14: gb_vl:*
15: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	468	100.0	468	11	AY890616 Synthetic
5	468	100.0	1025	6	AR630872 Sequence
6	468	100.0	1025	6	AX207818 Sequence
7	468	100.0	1282	6	BD211434 A novel i
8	468	100.0	1282	6	AR181994 Sequence
9	468	100.0	1282	6	AR221128 Sequence
10	468	100.0	1282	6	AR302956 Sequence
11	468	100.0	1288	6	AF201830 Homo sapi
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132	110.2	23.5	1802	6	CS033142	CS033142 Sequence	205	82.8	17.7	70869	10	AC024704	AC111146 Homo sapi
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136	110.2	23.5	1973	6	CS118896	CS118896 Sequence	209	71.2	15.2	6350	6	E55205	BD087375 Transgeni
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138	109.2	23.3	459	6	AX206836	AX206836 Sequence	211	71.2	15.2	6350	6	AX003692	AX003692 Sequence
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VERSION	BD124061.1	GI:23219006
KEYWORDS	JP 200250046-A/2.	
SOURCE	Homo sapiens (human)	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 468)	
AUTHORS	Shim, J.E.	
TITLE	DNA and polypeptide of IL-1-delta	
JOURNAL	Patent: JP 200250046-A 2 08-JAN-2002; IMMUNEX CORP	
COMMENT	OS Homo sapiens (human) PN JP 200250046-A/2 PD 08-JAN-2002 PF 08-JAN-1999 JP 2000527652 PR 09-JUN-1998 US 60/071074.01-JUN-1998 US 60/087393 PI JOHN ERNEST SIMS PC C12N15/09,C07K14/545,C07K16/24,C12N1/19,C12N1/21,C12N5/10, PC C12P21/08// PC C12M1/00,C12N5/00,C12N5/00 CC DNA and polypeptide of IL-1-delta FH Key Location/Qualifiers FT source 1..468 FT Location/Qualifiers 1..468 /organism="Homo sapiens (human)" /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"	
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ORIGIN		
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ACCESSION BD63573.1 GI:33073341
VERSION BD63573.1
KEYWORDS UP 2002533122-A/7.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo;
REFERENCE 1 (bases 1 to 468)
AUTHORS Goddard, A. and Pan, J.
TITLE IL-1 related polypeptides
JOURNAL Patent: JP 2002533122-A 2.08-OCT-2002;
GENENTECH INC
COMMENT OS Homo sapiens (human)
PN JP 2002533122-A/7
PD 08-OCT-2002
PF 22-DEC-1998 JP 2000591188
PR 23-DEC-1998 US 60/113430, 22-JAN-1999 US 60/116843 PR
13-APR-1999 US 60/129122
PI AUDREY GODDARD, JAMES PAN
PC C12N15/09, C07K14/475, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12N15/00, C12N5/00
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ORIGIN
Query Match 100.0%; Score 468; DB 6; Length 468;
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Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 181 GTCCAGGCTGGAAGCCAGTGTGTCATGTGGGGTGGGGGAGAGCCGACTTAACACTA 240
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QY 241 GAGCAGTGAACATCATGAGCTTATCTTGTGTCGAAGATCCAAGAGCTTCACTTC 300
DB 241 GAGCAGTGAACATCATGAGCTTATCTTGTGTCGAAGATCCAAGAGCTTCACTTC 300
QY 301 TACCGGCGGGAACATGGGGCTCACTCCAGCTTCAAGTGTGGCTGCTACCGGGCTGGTTC 360
DB 301 TACCGGCGGGAACATGGGGCTCACTCCAGCTTCAAGTGTGGCTGCTACCGGGCTGGTTC 360
QY 361 CTGTGACGCGTGTGAGAGCGGATCAGCTGTGCAAGTCAAGAGCTTCCGAGAAATGGT 420
DB 361 CTGTGACGCGTGTGAGAGCGGATCAGCTGTGCAAGTCAAGAGCTTCCGAGAAATGGT 420
QY 421 GGCTGGAATGCCCATCAAGACTTCTCACTTCCAGAGCTGTGACTAG 468
DB 421 GGCTGGAATGCCCATCAAGACTTCTCACTTCCAGAGCTGTGACTAG 468

RESULT 3
AF230377

LOCUS AF230377 468 bp mRNA linear PRI 01-NOV-2001
DEFINITION Homo sapiens interleukin-1 delta mRNA, complete cds.
ACCESSION AF230377
VERSION AF230377.1 GI:9651788
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo;
REFERENCE 1 (bases 1 to 468)
AUTHORS Debets, R., Timans, J.C., Homey, B., Zurawski, S., Sana, T.R., Lo, S.,
Wagner, J., Edwards, G., Clifford, T., Menon, S., Bazan, J.F. and
Kastelein, R.A.
TITLE Two novel IL-1 family members, IL-1 delta and IL-1 epsilon,
function as an antagonist and agonist of NF-kappa B activation
through the orphan IL-1 receptor-related protein 2
JOURNAL J. Immunol. 167 (3), 1440-1446 (2001)
11466363
2 (bases 1 to 468)
REFERENCE Kastelein, R.A., Timans, J.C., Sana, T., Debets, R. and Bazan, F.
TITLE Direct Submission Molecular Biology, DNAX Research Institute,
JOURNAL Submitted (01-FEB-2000) 901 California Ave, Palo Alto, CA 94304, USA
LOCATION/Qualifiers
FEATURES
source 1..468
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="2"
/map="2q"
1..468
/note="IL-1delta; cytokine"
/codon_start=1
/product="interleukin-1 delta"
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/db_xref="GI:9651789"
/translation="MVLGSLCPRMKDSALKVLYLHNNQLIAGGLHAGKVIKGEISV
VPRWMDASLPVILGVGSGSGLSCVGEPTLPEVIMELVIAKSKSFTFVR
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ORIGIN
Query Match 100.0%; Score 468; DB 8; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.9e-107;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTCTGAGTGGGGGCTGTGCTCCGANTGAAGAAGCTGGATTGAAGTCTTAT 60
DB 1 ATGGTCTGAGTGGGGGCTGTGCTCCGANTGAAGAAGCTGGATTGAAGTCTTAT 60
QY 61 CTGCATATAACCAAGCTTCTAGCTGAGAGGCTGCATGCAAGAGTCAATTAAGTGAA 120
DB 61 CTGCATATAACCAAGCTTCTAGCTGAGAGGCTGCATGCAAGAGTCAATTAAGTGAA 120
QY 121 GAGATCAGCGTGTGCTCCCAATCGGTGCTGATGCCAGCTGTCCCGTCATCTGGGT 180
DB 121 GAGATCAGCGTGTGCTCCCAATCGGTGCTGATGCCAGCTGTCCCGTCATCTGGGT 180
QY 181 GTCCAGGCTGGAAGCCAGTGTGTCATGTGGGGTGGGGGAGAGCCGACTTAACACTA 240
DB 181 GTCCAGGCTGGAAGCCAGTGTGTCATGTGGGGTGGGGGAGAGCCGACTTAACACTA 240
QY 241 GAGCAGTGAACATCATGAGCTTATCTTGTGTCGAAGATCCAAGAGCTTCACTTC 300
DB 241 GAGCAGTGAACATCATGAGCTTATCTTGTGTCGAAGATCCAAGAGCTTCACTTC 300
QY 301 TACCGGCGGGAACATGGGGCTCACTCCAGCTTCAAGTGTGGCTGCTACCGGGCTGGTTC 360
DB 301 TACCGGCGGGAACATGGGGCTCACTCCAGCTTCAAGTGTGGCTGCTACCGGGCTGGTTC 360
QY 361 CTGTGACGCGTGTGAGAGCGGATCAGCTGTGCAAGTCAAGAGCTTCCGAGAAATGGT 420
DB 361 CTGTGACGCGTGTGAGAGCGGATCAGCTGTGCAAGTCAAGAGCTTCCGAGAAATGGT 420

Oy 421 GGCCTGAATGCCCCCATCAGACTTCTTACTTCCAGAGTGGAGTAG 468
 Db 421 GGCCTGAATGCCCCCATCAGACTTCTTACTTCCAGAGTGGAGTAG 468
 RESULT 4
 AY890616
 LOCUS 468 bp mRNA linear SYN 29-MAR-2005
 DEFINITION Synthetic construct Homo sapiens clone FLH141295.01X Interleukin-11
 ACCESSION AY890616
 VERSION AY890616.1 GI:61364535
 KEYWORDS Human ORF project.
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 468)
 Hines, L., Rolfe, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F.,
 AUTHORS Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
 Williamson, J. and Labaer, J.
 TITLE Cloning of human full-length CDS in Creator (TM) recombinational
 vector system
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 468)
 Hines, L., Rolfe, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F.,
 AUTHORS Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
 Williamson, J. and Labaer, J.
 TITLE Direct Submission
 JOURNAL Submitted (04-JAN-2005) Biological Chemistry and Molecular
 Pharmacology, Harvard-Institute of Proteomics, 320 Charles St.,
 Cambridge, MA 02141, USA
 COMMENT This CDS clone is a part of a collection of human full-length
 expression clones generated by Harvard Institute of Proteomics.
 This ORF clone has been cloned with normalized stop-codon. The CDS
 has been directionally cloned using BD in-Fusion (TM) cloning system
 between the SalI and HindIII sites of the pDNR-Dual vector.
 Additional sequences in the clone: 'ACC' after SalI site and
 before 'ATG' to provide Kozak consensus sequence. Each clone is
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 SOURCE
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 /mol_type="mRNA"
 /db_xref="taxon:32630"
 /clone="FLH141295.01X"
 /lab_host="Escherichia coli DH5alpha TI resistant"
 /note="derived from MGC template"
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 /gene="IL1F5"
 1..468
 /gene="IL1F5"
 /note="delta"
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 /transl_table=1
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 /db_xref="GI:61364536"
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 ORIGIN
 Query Match 100.0%; Score 468; DB 11; Length 468;
 Best Local Similarity 100.0%; Pred. No. 1.9e-107;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 ATGCTCTGAGTGGCGCTGCTTCGGAATGAAGACTGGCAATGAAGTCTTAT 60
 Db 1 ATGCTCTGAGTGGCGCTGCTTCGGAATGAAGACTGGCAATGAAGTCTTAT 60
 Oy 61 CTGCAATATAACGAGCTTCTAGCTGAGAGGCTGCATGAGGAAGTCAATTAAGGTGAA 120
 Db 61 CTGCAATATAACGAGCTTCTAGCTGAGAGGCTGCATGAGGAAGTCAATTAAGGTGAA 120

Db 61 CTGCAATATAACGAGCTTCTAGCTGAGAGGCTGCATGAGGAAGTCAATTAAGGTGAA 120
 Oy 121 GAGATCAGCGTGTGCTCCCAATCGGTGGTGGATGCGACCTGTCCCGGTATCCTGGGT 180
 Db 121 GAGATCAGCGTGTGCTCCCAATCGGTGGTGGATGCGACCTGTCCCGGTATCCTGGGT 180
 Oy 181 GTCCAGGGTGAAGCCAGATGCTGTGATGAGGGTGGGGCAGAGCCGACTTAACACTA 240
 Db 181 GTCCAGGGTGAAGCCAGATGCTGTGATGAGGGTGGGGCAGAGCCGACTTAACACTA 240
 Oy 241 GAGCAGAGTGAACATCATGAGAGCTTATCTGTGTCGCAAGAAATCCAGAGCTTCACTTC 300
 Db 241 GAGCAGAGTGAACATCATGAGAGCTTATCTGTGTCGCAAGAAATCCAGAGCTTCACTTC 300
 Oy 301 TACCGGCGGGGACATGAGGGCTCACTCCAGCTTCCAGATGTGGTCTACCCGGGCTGGTTC 360
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 Oy 361 CTGTGACAGGTGCTGGAAGCCGATCAGCTGTGACAGCTCACCCAGCTTCCGAGATGAT 420
 Db 361 CTGTGACAGGTGCTGGAAGCCGATCAGCTGTGACAGCTCACCCAGCTTCCGAGATGAT 420
 Oy 421 GGCCTGAATGCCCCCATCAGACTTCTTACTTCCAGAGTGGAGTAG 468
 Db 421 GGCCTGAATGCCCCCATCAGACTTCTTACTTCCAGAGTGGAGTAG 468
 RESULT 5
 AR630872
 LOCUS Sequence 1 from patent US 6843987.
 DEFINITION AR630872
 ACCESSION AR630872
 VERSION AR630872.1 GI:59769325
 KEYWORDS
 ORGANISM Unknown.
 SOURCE Unknown.
 REFERENCE 1 (bases 1 to 1025)
 AUTHORS Deebert, J.E.M.A., Timans, J.C., Bazan, J.F. and Kastelein, R.A.
 TITLE Mammalian cytokines; receptors; related reagents and methods
 JOURNAL Patent: US 6843987-A 1 18-JAN-2005;
 Schering Corporation; Kenilworth, NJ
 FEATURES
 SOURCE
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 /organism="unknown"
 /mol_type="genomic DNA"
 ORIGIN
 Query Match 100.0%; Score 468; DB 6; Length 1025;
 Best Local Similarity 100.0%; Pred. No. 1.8e-107;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 ATGCTCTGAGTGGCGCTGCTTCGGAATGAAGACTGGCAATGAAGTCTTAT 60
 Db 58 ATGCTCTGAGTGGCGCTGCTTCGGAATGAAGACTGGCAATGAAGTCTTAT 117
 Oy 61 CTGCAATATAACGAGCTTCTAGCTGAGAGGCTGCATGAGGAAGTCAATTAAGGTGAA 120
 Db 118 CTGCAATATAACGAGCTTCTAGCTGAGAGGCTGCATGAGGAAGTCAATTAAGGTGAA 177
 Oy 121 GAGATCAGCGTGTGCTCCCAATCGGTGGTGGATGCGACCTGTCCCGGTATCCTGGGT 180
 Db 178 GAGATCAGCGTGTGCTCCCAATCGGTGGTGGATGCGACCTGTCCCGGTATCCTGGGT 237
 Oy 181 GTCCAGGGTGAAGCCAGATGCTGTGATGAGGGTGGGGCAGAGCCGACTTAACACTA 240
 Db 238 GTCCAGGGTGAAGCCAGATGCTGTGATGAGGGTGGGGCAGAGCCGACTTAACACTA 297
 Oy 241 GAGCAGAGTGAACATCATGAGAGCTTATCTGTGTCGCAAGAAATCCAGAGCTTCACTTC 300
 Db 298 GAGCAGAGTGAACATCATGAGAGCTTATCTGTGTCGCAAGAAATCCAGAGCTTCACTTC 357
 Oy 301 TACCGGCGGGGACATGAGGGCTCACTCCAGCTTCCAGATGTGGTCTACCCGGGCTGGTTC 360

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Db      358 TACCGGGGAGCATTGGGCTCACCCTCAGCTTGAGTGGGTGCTACCCGGGTGTTTC 417
Qy      361 CTGTGACGGTGCCTGAGCCGATCAGCTGTGCTCAGACTCAACCCAGCTTCCGAGATGT 420
Db      418 CTGTGACGGTGCCTGAGCCGATCAGCTGTGCTCAGACTCAACCCAGCTTCCGAGATGT 477
Qy      421 GGCTGGAATGCCCATCAGACTTCTACTTCCAGAGTGTGACTAG 468
Db      478 GGCTGGAATGCCCATCAGACTTCTACTTCCAGAGTGTGACTAG 525

RESULT 6
LOCUS   AX207818 1025 bp DNA linear PAT 31-AUG-2001
DEFINITION Sequence 1 from Patent WO0157219.
ACCESSION AX207818
VERSION   AX207818.1 GI:15422465
KEYWORDS
SOURCE   unidentified
ORGANISM unidentified
          unclassified sequences.
REFERENCE
  1 Debeets,J.E., Timans,J.C., Bazan,J.F. and Kastelein,R.A.
    Mammalian interleukin-1-delta and -epsilon. Their use in
    therapeutic and diagnostic methods.
    Patent: WO 0157219-A 1 09-AUG-2001;
    SCHERING CORPORATION (US)
FEATURES
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    Homo sapiens"
    58..525
    /note="unnamed protein product"
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    /db_xref="GI:15422465"
    /translation="MVLISGALCFPMKDSALKVLYLHNNQLIAGGLHAGKVIKGEISV
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    RDMGLTSSFESAAYPMFLCTVPEADQPVRLTQLPENGWNNAPITDVFQCD"

ORIGIN
Query Match 100.0%; Score 468; DB 6; Length 1025;
Best Local Similarity 100.0%; Pred. No. 1,8e-107;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGGCTCTGAGTGGGGGCTGTGCTCCGAATGAAGGCTGGCATTGAAGTCTTTAT 60
Db      58 ATGGCTCTGAGTGGGGGCTGTGCTCCGAATGAAGGCTGGCATTGAAGTCTTTAT 117
Qy      61 CTGCATATAACCAAGCTTTAGCTGAGAGGCTGCATGAGGAAAGTCAATTAAGGTGAA 120
Db      118 CTGCATATAACCAAGCTTTAGCTGAGAGGCTGCATGAGGAAAGTCAATTAAGGTGAA 177
Qy      121 GAGATCAGCGTGGTCCCAATCGGTGGTGGATGCCAGCTGTCCCCCGTATCTGGGT 180
Db      121 GAGATCAGCGTGGTCCCAATCGGTGGTGGATGCCAGCTGTCCCCCGTATCTGGGT 237
Qy      178 GAGATCAGCGTGGTCCCAATCGGTGGTGGATGCCAGCTGTCCCCCGTATCTGGGT 237
Db      181 GTCAGAGGTGAGAGCCAGTGCCTGTCAATGTGGGGTGGGGGAGAGCCGACTTAACACTA 240
Qy      238 GTCAGAGGTGAGAGCCAGTGCCTGTCAATGTGGGGTGGGGGAGAGCCGACTTAACACTA 297
Db      241 GAGCAGGTGAACATCATGAGCTCTATCTTGTGTCGAAGAAATCCAAGAGCTTCACTTC 300
Qy      298 GAGCAGGTGAACATCATGAGCTCTATCTTGTGTCGAAGAAATCCAAGAGCTTCACTTC 357
Db      301 TACCGGGGAGCATTGGGCTCACTTCCAGCTTCCAGTGGCTGCTCAACCGGGGCTGTTTC 360
Qy      358 TACCGGGGAGCATTGGGCTCACTTCCAGCTTCCAGTGGCTGCTCAACCGGGGCTGTTTC 417

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Qy      361 CTGTGACGGTGCCTGAGCCGATCAGCTGTGCTCAGACTCAACCCAGCTTCCGAGATGT 420
Db      418 CTGTGACGGTGCCTGAGCCGATCAGCTGTGCTCAGACTCAACCCAGCTTCCGAGATGT 477
Qy      421 GGCTGGAATGCCCATCAGACTTCTACTTCCAGAGTGTGACTAG 468
Db      478 GGCTGGAATGCCCATCAGACTTCTACTTCCAGAGTGTGACTAG 525

RESULT 7
LOCUS   BD211434 1282 bp DNA linear PAT 17-JUL-2003
DEFINITION A novel interleukin-1 receptor antagonist and uses thereof.
ACCESSION BD211434
VERSION   BD211434.1 GI:33021204
KEYWORDS JP 2002510492-A/3.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homiidae; Homo.
REFERENCE
  1 (bases 1 to 1282)
  Ford,J. and Pace,A
  A novel interleukin-1 receptor antagonist and uses thereof
  Patent: JP 2002510492-A 3 09-APR-2002
  HYSBO INC
COMMENT   OS Homo sapiens (human)
          PN JP 2002510492-A/3
          PD 09-APR-2002 JP 2000542457
          PF 05-APR-1998 US 09/055010,15-MAY-1998 US 09/079909 PR
          PR 03-APR-1998 US 09/082364,19-JUN-1998 US 09/099818 PR
          20-MAY-1998 US 09/127698,13-JAN-1999 US 09/229591 PR
          31-JUL-1998 US 09/127698,13-JAN-1999 US 09/229591 PR
          17-FEB-1999 US 09/251370
          PI JOHN FORD, ANN PACE
          PC C12N15/09,A61K38/00,C07K14/52,C07K14/545,C07K16/24,C12N1/15,
          PC C12N1/19,
          PC C12N1/21,C12N5/10,C12Q1/68,G01N33/50,G01N33/566,G01N33/68, PC
          C12N15/00,
          PC A61K37/02,C12N5/00
          CC A novel interleukin-1 receptor antagonist and uses thereof FH
          Key Location/Qualifiers
          FT source 1..1282
          Location/Qualifiers
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            /organism="Homo sapiens (human)".
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            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 468; DB 6; Length 1282;
Best Local Similarity 100.0%; Pred. No. 1,8e-107;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGGCTCTGAGTGGGGGCTGTGCTCCGAATGAAGGCTGGCATTGAAGTCTTTAT 60
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Db      121 GAGATCAGCGTGGTCCCAATCGGTGGTGGATGCCAGCTGTCCCCCGTATCTGGGT 252
Qy      178 GAGATCAGCGTGGTCCCAATCGGTGGTGGATGCCAGCTGTCCCCCGTATCTGGGT 252
Db      181 GTCAGAGGTGAGAGCCAGTGCCTGTCAATGTGGGGTGGGGGAGAGCCGACTTAACACTA 240
Qy      238 GTCAGAGGTGAGAGCCAGTGCCTGTCAATGTGGGGTGGGGGAGAGCCGACTTAACACTA 312
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Db 313 GAGCAGTGAACATCATGAGCTCTATCTTGTGTCAGGAAGATCCAGAGCTTCACTTC 372
Qy 301 TACCGGGGGGACATGGGGGCTCACTCCAGCTTTCAGATGGCTGCTACCCGGGCTGGTTC 360
Db 373 TACCGGGGGGACATGGGGGCTCACTCCAGCTTTCAGATGGCTGCTACCCGGGCTGGTTC 432
Qy 361 CTGTGACGCGTCTGTAAGCCGATCAGCTGTGACACTCAACCCAGCTTCCGAGATGGT 420
Db 433 CTGTGACGCGTCTGTAAGCCGATCAGCTGTGACACTCAACCCAGCTTCCGAGATGGT 492
Qy 421 GCGTGAATGCCCCCATCAGACTTCTACTTCCAGAGTGTAGT 468
Db 493 GCGTGAATGCCCCCATCAGACTTCTACTTCCAGAGTGTAGT 540

RESULT 8
AR181994 1282 bp DNA linear PAT 20-APR-2002
LOCUS AR181994
DEFINITION Sequence 4 from patent US 6337072.
ACCESSION AR181994
VERSION AR181994.1 GI:20224910
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclasiified.

REFERENCE 1 (bases 1 to 1282)
AUTHORS Ford, J. and Pace, A.
TITLE Interleukin-1 receptor antagonist and recombinant production thereof
JOURNAL Patent: US 6337072-A 4 08-JAN-2002;
FEATURES Location/Qualifiers
source 1. 1282
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 468; DB 6; Length 1282;
Best Local Similarity 100.0%; Pred. No. 1.8e-107;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTGGGCAATTGAAGTCTTTAT 60
Db 73 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTGGGCAATTGAAGTCTTTAT 132
Qy 61 CTGATATATTAACCACTTCTAGCTGAGAGGCTGCATGAGAGGAAGTATTAAAGTAA 120
Db 133 CTGATATATTAACCACTTCTAGCTGAGAGGCTGCATGAGAGGAAGTATTAAAGTAA 192
Qy 121 GAGATCAGCGTGTCCCAATCGGTGGCTGATGCGAGCTGTCCCGCTCATCTGGGT 180
Db 193 GAGATCAGCGTGTCCCAATCGGTGGCTGATGCGAGCTGTCCCGCTCATCTGGGT 252
Qy 181 GTCCAGGGTGAAGCCAGTGCCTGTCAATGTGGGGTGGGCGAGAGCCGACTTAACATA 240
Db 253 GTCCAGGGTGAAGCCAGTGCCTGTCAATGTGGGGTGGGCGAGAGCCGACTTAACATA 312
Qy 241 GAGCAGTGAACATCATGAGACTCTATTGTGTCCAGAGAACTCAAGACTTCACTTC 300
Db 313 GAGCAGTGAACATCATGAGACTCTATTGTGTGTCCAGAGAACTCAAGAGCTTCACTTC 372
Qy 301 TACCGGGGGGACATGGGGGCTCACTCCAGCTTTCAGATGGCTGCTACCCGGGCTGGTTC 360
Db 373 TACCGGGGGGACATGGGGGCTCACTCCAGCTTTCAGATGGCTGCTACCCGGGCTGGTTC 432
Qy 361 CTGTGACGCGTCTGTAAGCCGATCAGCTGTGACACTCAACCCAGCTTCCGAGATGGT 420
Db 433 CTGTGACGCGTCTGTAAGCCGATCAGCTGTGACACTCAACCCAGCTTCCGAGATGGT 492
Qy 421 GCGTGAATGCCCCCATCAGACTTCTACTTCCAGAGTGTAGT 468
Db 493 GCGTGAATGCCCCCATCAGACTTCTACTTCCAGAGTGTAGT 540

RESULT 9
AR221128 1282 bp DNA linear PAT 26-SEP-2002
LOCUS AR221128
DEFINITION Sequence 4 from patent US 6426191.
ACCESSION AR221128
VERSION AR221128.1 GI:23328013
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclasiified.

REFERENCE 1 (bases 1 to 1282)
AUTHORS Ford, J. and Pace, A.
TITLE Assays involving an IL-1 receptor antagonist
JOURNAL Patent: US 6426191-A 4 30-JUL-2002;
FEATURES Location/Qualifiers
source 1. 1282
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 468; DB 6; Length 1282;
Best Local Similarity 100.0%; Pred. No. 1.8e-107;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTGGGCAATTGAAGTCTTTAT 60
Db 73 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTGGGCAATTGAAGTCTTTAT 132
Qy 61 CTGATATATTAACCACTTCTAGCTGAGAGGCTGCATGAGAGGAAGTATTAAAGTAA 120
Db 133 CTGATATATTAACCACTTCTAGCTGAGAGGCTGCATGAGAGGAAGTATTAAAGTAA 192
Qy 121 GAGATCAGCGTGTCCCAATCGGTGGCTGATGCGAGCTGTCCCGCTCATCTGGGT 180
Db 193 GAGATCAGCGTGTCCCAATCGGTGGCTGATGCGAGCTGTCCCGCTCATCTGGGT 252
Qy 181 GTCCAGGGTGAAGCCAGTGCCTGTCAATGTGGGGTGGGCGAGAGCCGACTTAACATA 240
Db 253 GTCCAGGGTGAAGCCAGTGCCTGTCAATGTGGGGTGGGCGAGAGCCGACTTAACATA 312
Qy 241 GAGCAGTGAACATCATGAGACTCTATTGTGTCCAGAGAACTCAAGAGCTTCACTTC 300
Db 313 GAGCAGTGAACATCATGAGACTCTATTGTGTGTCCAGAGAACTCAAGAGCTTCACTTC 372
Qy 301 TACCGGGGGGACATGGGGGCTCACTCCAGCTTTCAGATGGCTGCTACCCGGGCTGGTTC 360
Db 373 TACCGGGGGGACATGGGGGCTCACTCCAGCTTTCAGATGGCTGCTACCCGGGCTGGTTC 432
Qy 361 CTGTGACGCGTCTGTAAGCCGATCAGCTGTGACACTCAACCCAGCTTCCGAGATGGT 420
Db 433 CTGTGACGCGTCTGTAAGCCGATCAGCTGTGACACTCAACCCAGCTTCCGAGATGGT 492
Qy 421 GCGTGAATGCCCCCATCAGACTTCTACTTCCAGAGTGTAGT 468
Db 493 GCGTGAATGCCCCCATCAGACTTCTACTTCCAGAGTGTAGT 540

RESULT 10
AR302956 1282 bp DNA linear PAT 12-JUN-2003
LOCUS AR302956
DEFINITION Sequence 4 from patent US 6541623.
ACCESSION AR302956
VERSION AR302956.1 GI:31691556
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclasiified.

REFERENCE 1 (bases 1 to 1282)
AUTHORS Ford, J., Ho, A.S.Y. and Pace, A.
TITLE Interleukin-1 receptor antagonist and uses thereof
JOURNAL Patent: US 6541623-A 4 01-APR-2003;
Hyseq, Inc.; Sunnyvale, CA

FEATURES
source

Location/Qualifiers
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/organism="unknown"
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ORIGIN

Query Match 100.0%; Score 468; DB 6; Length 1282;
Best Local Similarity 100.0%; Pred. No. 1.8e-107;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTCTAGAGTGGGGGCGCTGTGCTTCCGAATGAAGAGCTCGCATTTGAAGTCTTTAT 60
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QY 61 CTGCATTAATACCAAGCTTTCTAGCTGAGAGGCTGATGACAGGAAAGTCAATTAAGTGAA 120
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QY 121 GAGATCAGCGTGGTCCCAATCGGTGAGTGCAGACCTGTCCCGCTCATCTGGGT 180
DB 193 GAGATCAGCGTGGTCCCAATCGGTGAGTGCAGACCTGTCCCGCTCATCTGGGT 252
QY 181 GTCAGAGGTGGAAGCCAGTGCCTGTCAATGAGGGTGGGGCAGAGCCGACTTAACACTA 240
DB 253 GTCAGAGGTGGAAGCCAGTGCCTGTCAATGAGGGTGGGGCAGAGCCGACTTAACACTA 312
QY 241 GAGCCATGAACATCATGAGCTCTATCTTGTGTCAGAGAAATCCAGAGCTTCACTTC 300
DB 313 GAGCCATGAACATCATGAGCTCTATCTTGTGTCAGAGAAATCCAGAGCTTCACTTC 372
QY 301 TACCGGCGGAGCAATGGGGCTTCACTCGAGCTTCAGTCCGCTGCTTCCCGGCTGGTTC 360
DB 373 TACCGGCGGAGCAATGGGGCTTCACTCGAGCTTCAGTCCGCTGCTTCCCGGCTGGTTC 432
QY 361 CTGTGACGCGTGTCTGAGACCGGATCAGCTGTGACACTCACCCAGCTTCCGAGATGCT 420
DB 433 CTGTGACGCGTGTCTGAGACCGGATCAGCTGTGACACTCACCCAGCTTCCGAGATGCT 492
QY 421 GGTGGAATGCCCCCATCAGACTTCTACTTCAGAGAGTGTACTAG 468
DB 493 GGTGGAATGCCCCCATCAGACTTCTACTTCAGAGAGTGTACTAG 540

RESULT 11

AX069307

LOCUS AX069307 1282 bp DNA linear PAT 25-JAN-2001
DEFINITION Sequence 4 from Patent WO0102571.
ACCESSION AX069307
VERSION AX069307.1 GI:12579179

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

1 Ford, J. and Pace, A.,
A interleukin-1 receptor antagonist and uses thereof
Patent: WO 0102571-A 4 11-JAN-2001;
JOURNAL HYSEQ, INC. (US)

FEATURES
source

CDS

Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 468; DB 6; Length 1282;
Best Local Similarity 100.0%; Pred. No. 1.8e-107;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTCTAGAGTGGGGGCGCTGTGCTTCCGAATGAAGAGCTCGCATTTGAAGTCTTTAT 60
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QY 61 CTGCATTAATACCAAGCTTTCTAGCTGAGAGGCTGATGACAGGAAAGTCAATTAAGTGAA 120
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QY 121 GAGATCAGCGTGGTCCCAATCGGTGAGTGCAGACCTGTCCCGCTCATCTGGGT 180
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QY 181 GTCAGAGGTGGAAGCCAGTGCCTGTCAATGAGGGTGGGGCAGAGCCGACTTAACACTA 240
DB 253 GTCAGAGGTGGAAGCCAGTGCCTGTCAATGAGGGTGGGGCAGAGCCGACTTAACACTA 312
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DB 313 GAGCCATGAACATCATGAGCTCTATCTTGTGTCAGAGAAATCCAGAGCTTCACTTC 372
QY 301 TACCGGCGGAGCAATGGGGCTTCACTCGAGCTTCAGTCCGCTGCTTCCCGGCTGGTTC 360
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QY 361 CTGTGACGCGTGTCTGAGACCGGATCAGCTGTGACACTCACCCAGCTTCCGAGATGCT 420
DB 433 CTGTGACGCGTGTCTGAGACCGGATCAGCTGTGACACTCACCCAGCTTCCGAGATGCT 492
QY 421 GGTGGAATGCCCCCATCAGACTTCTACTTCAGAGAGTGTACTAG 468
DB 493 GGTGGAATGCCCCCATCAGACTTCTACTTCAGAGAGTGTACTAG 540

RESULT 12

AF201830

LOCUS AF201830 1288 bp mRNA linear PRI 16-JAN-2000
DEFINITION Homo sapiens FL11 delta mRNA, complete cds.
ACCESSION AF201830
VERSION AF201830.1 GI:6694387

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 1288)
Smith, D.E., Renshaw, B.R., Ketchum, R.R., Kudin, M., Garke, K.E. and
Sims, J.B.,
Four new members expand the interleukin-1 superfamily
Submitted (04-NOV-1999) Molecular Genetics, Immunex Corporation, 51
University Street, Seattle, WA 98101, USA

REFERENCE

2 (bases 1 to 1288)
Sims, J.B.
Direct Submission
Submitted (04-NOV-1999) Molecular Genetics, Immunex Corporation, 51
University Street, Seattle, WA 98101, USA

FEATURES
source

CDS

Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 468; DB 8; Length 1288;
Best Local Similarity 100.0%; Pred. No. 1.8e-107; Indels 0; Gaps 0;
Matches 468; Conservative 0; Mismatches 0;

QY 1 ATGGTCTGAGTGGGGCGCTGTGCTTCGAAATGAAGACTCGGCAATGAAGTCTTTAT 60
DB 28 ATGGTCTGAGTGGGGCGCTGTGCTTCGAAATGAAGACTCGGCAATGAAGTCTTTAT 87
QY 61 CTGATATTAACCAAGCTTCTAGCTGAGAGGCTGCATGAGGAAAGTCAATTAAGTGA 120
DB 88 CTGATATTAACCAAGCTTCTAGCTGAGAGGCTGCATGAGGAAAGTCAATTAAGTGA 147
QY 121 GAGATCAGCGTGTCCCAATCGGTGGCTGATGCAAGCTGTCCCGTATCTGGGT 180
DB 148 GAGATCAGCGTGTCCCAATCGGTGGCTGATGCAAGCTGTCCCGTATCTGGGT 207
QY 181 GTCCAGGCTGGAAGCCAGTGTCTGTCAATGAGGCTGAGAGCCGACTTAACACTA 240
DB 208 GTCCAGGCTGGAAGCCAGTGTCTGTCAATGAGGCTGAGAGCCGACTTAACACTA 267
QY 241 GAGCAGTGAACATCATGAGACTCTATCTGTGTGTCGCAAGAACTCAAGCTTTC 300
DB 268 GAGCAGTGAACATCATGAGACTCTATCTGTGTGTCGCAAGAACTCAAGCTTTC 327
QY 301 TACCGGGGGGACATGGGGCTCACTCAAGCTTGAAGTGGCTGCTACCGGGGCTGGTTC 360
DB 328 TACCGGGGGGACATGGGGCTCACTCAAGCTTGAAGTGGCTGCTACCGGGGCTGGTTC 387
QY 361 CTGTGACAGGTGCTGGAAGCCGATCAGCTGTGCACTCAACCAAGCTTCCGAGAAATGT 420
DB 388 CTGTGACAGGTGCTGGAAGCCGATCAGCTGTGCACTCAACCAAGCTTCCGAGAAATGT 447
QY 421 GGTGGAATGCCCCCATCAAGACTTCTACTTCCAGAGTGTACTAG 468
DB 448 GGTGGAATGCCCCCATCAAGACTTCTACTTCCAGAGTGTACTAG 495

RESULT 13

AX080389 2563 bp DNA linear PAT 22-FEB-2001

LOCUS AX080389 2563 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 1 from Patent WO0105974.
ACCESSION AX080389
VERSION AX080389.1 GI:13159840

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE

1 Nicklin M. and Barton L.
The 11-11 gene and polypeptide products
Patent: WO 0105974-A 1 25-JAN-2001

JOURNAL Interleukin Genetics, Inc. (US)

FEATURES Location/Qualifiers

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ORIGIN

Query Match 100.0%; Score 468; DB 6; Length 2563;
Best Local Similarity 100.0%; Pred. No. 1.8e-107; Indels 0; Gaps 0;
Matches 468; Conservative 0; Mismatches 0;

QY 1 ATGGTCTGAGTGGGGCGCTGTGCTTCGAAATGAAGACTCGGCAATGAAGTCTTTAT 60

DB 30 ATGGTCTGAGTGGGGCGCTGTGCTTCGAAATGAAGACTCGGCAATGAAGTCTTTAT 89

QY 61 CTGATATTAACCAAGCTTCTAGCTGAGAGGCTGCATGAGGAAAGTCAATTAAGTGA 120

DB 90 CTGATATTAACCAAGCTTCTAGCTGAGAGGCTGCATGAGGAAAGTCAATTAAGTGA 149

QY 121 GAGATCAGCGTGTCCCAATCGGTGGCTGATGCAAGCTGTCCCGTATCTGGGT 180

DB 150 GAGATCAGCGTGTCCCAATCGGTGGCTGATGCAAGCTGTCCCGTATCTGGGT 209

QY 181 GTCCAGGCTGGAAGCCAGTGTCTGTCAATGAGGCTGAGAGCCGACTTAACACTA 240

DB 210 GTCCAGGCTGGAAGCCAGTGTCTGTCAATGAGGCTGAGAGCCGACTTAACACTA 269

QY 241 GAGCAGTGAACATCATGAGACTCTATCTGTGTGTCGCAAGAACTCAAGCTTTC 300

DB 270 GAGCAGTGAACATCATGAGACTCTATCTGTGTGTCGCAAGAACTCAAGCTTTC 329

QY 301 TACCGGGGGGACATGGGGCTCACTCAAGCTTGAAGTGGCTGCTACCGGGGCTGGTTC 360

DB 330 TACCGGGGGGACATGGGGCTCACTCAAGCTTGAAGTGGCTGCTACCGGGGCTGGTTC 389

QY 361 CTGTGACAGGTGCTGGAAGCCGATCAGCTGTGCACTCAACCAAGCTTCCGAGAAATGT 420

DB 390 CTGTGACAGGTGCTGGAAGCCGATCAGCTGTGCACTCAACCAAGCTTCCGAGAAATGT 449

QY 421 GGTGGAATGCCCCCATCAAGACTTCTACTTCCAGAGTGTACTAG 468

DB 450 GGTGGAATGCCCCCATCAAGACTTCTACTTCCAGAGTGTACTAG 497

RESULT 14

AX092420 2598 bp DNA linear PAT 21-MAR-2001

LOCUS AX092420 2598 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 151 from Patent WO0116318.
ACCESSION AX092420
VERSION AX092420.1 GI:13444524

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE

1 Baton, D.L., Filvaroff, E., Gerritsen, M.E., Goddard, A.,
GODOWSKI, P.J., Grimaldi, C.J., Gurney, A.L., Watanabe, C.K. and
Wood, W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same

JOURNAL Patent: WO 0116318-A 151 08-MAR-2001;
Genentech, Inc. (US)

FEATURES Location/Qualifiers

source 1..2598
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ORIGIN

Query Match 100.0%; Score 468; DB 6; Length 2598;
Best Local Similarity 100.0%; Pred. No. 1.8e-107; Indels 0; Gaps 0;
Matches 468; Conservative 0; Mismatches 0;

QY 1 ATGGTCTGAGTGGGGCGCTGTGCTTCGAAATGAAGACTCGGCAATGAAGTCTTTAT 60

DB 67 ATGGTCTGAGTGGGGCGCTGTGCTTCGAAATGAAGACTCGGCAATGAAGTCTTTAT 126

QY 61 CTGATATTAACCAAGCTTCTAGCTGAGAGGCTGCATGAGGAAAGTCAATTAAGTGA 120

DB 127 CTGATATTAACCAAGCTTCTAGCTGAGAGGCTGCATGAGGAAAGTCAATTAAGTGA 186

QY 121 GAGATCAGCGTGTCCCAATCGGTGGCTGATGCAAGCTGTCCCGTATCTGGGT 180

Db 187 GAGATCAGCGTGGTCCCCAATCGGTGGTGGATGCGACGCTGTGCCCCGCTCATCTGGGT 246
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Db 247 GTCCAGGGTGGAAAGCCAGTGTGCTGTATGTGGGGTGGGGGCAAGAGCCGACTTAAACCTA 306
Qy 241 GAGCCAGTGAACATCATGAGCTGTATCTTGTGTGCCAAGGAATCCAGAGCTTCACTTC 300
Db 307 GAGCCAGTGAACATCATGAGCTGTATCTTGTGTGCCAAGGAATCCAGAGCTTCACTTC 366
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Db 427 CTGTGACAGGTGCTGTGAAGCCGATTCAGCTTGTCACTCAACCCAGCTTCCGAGAAATGT 486
Qy 421 GGCTGGAATGCCCCCATCACAGACTTCTTACTTCCAGAGTGTGACTAG 468
Db 487 GGCTGGAATGCCCCCATCACAGACTTCTTACTTCCAGAGTGTGACTAG 534

RESULT 15
AX454730 2598 bp DNA linear PAT 06-JUL-2002
LOCUS Sequence 315 from Patent WO0208284.
DEFINITION AX454730
ACCESSION AX454730 GI:21713989
VERSION AX454730.1
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0208284-A 315 31-JAN-2002;
Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone
(US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard,
Audrey (US); Godowski, Paul J. (US); Gurney, Austin L. (US);
Hillan, Kenneth J. (US); Marsters, Scott A. (US); Pan, James (US)
; Paoni, Nicholas F. (US); Stephan, Jean-Philippe F. (US);
Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William
I. (US)

FEATURES
source location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 468; DB 6; Length 2598;
Best Local Similarity 100.0%; Pred. No. 1.8e-107;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCTCTGAGTGGGGGCTGTGCTCCGATGGAAGACTCGGACTTGAAGTCTTTAT 60
Db 67 ATGGCTCTGAGTGGGGGCTGTGCTCCGATGGAAGACTCGGACTTGAAGTCTTTAT 126
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Qy 181 GTCCAGGGTGGAAAGCCAGTGTGCTGTATGTGGGGTGGGGGCAAGAGCCGACTTAAACCTA 240
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Db 487 GGCTGGAATGCCCCCATCACAGACTTCTTACTTCCAGAGTGTGACTAG 534

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AX491208 2598 bp DNA linear PAT 16-AUG-2002
LOCUS Sequence 315 from Patent WO020690.
DEFINITION AX491208
ACCESSION AX491208 GI:22323941
VERSION AX491208.1
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 020690-A 315 03-JAN-2002;
Genentech, Inc. (US)

FEATURES
source location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 468; DB 6; Length 2598;
Best Local Similarity 100.0%; Pred. No. 1.8e-107;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCTCTGAGTGGGGGCTGTGCTCCGATGGAAGACTCGGACTTGAAGTCTTTAT 60
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Qy 61 CTGCATATAACCAAGCTTCTAGCTGAGAGGCTGCATGCAAGGAAAGTCAATTAAGGTAA 120
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 AY359117
 LOCUS AY359117 2598 bp mRNA linear PRI 03-OCT-2003
 DEFINITION Homo sapiens clone DNA96787 IL1H1 (UNQ1896) mRNA, complete cds.
 ACCESSION AY359117 GI:37183350
 VERSION AY359117.1 GI:37183350
 KEYWORDS FLI CDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE 1 (bases 1 to 2598)
 Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,
 Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,
 Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Haas, P.E.,
 Heidens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S.,
 Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,
 Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V.,
 Stinson, J., Vagstad, A., Vandlen, R., Watanabe, C., Wleand, D., Woods, K.,
 Xie, M.H., Yamaura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,
 Goddard, A., Wood, W.I. and Godowski, P.
 The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 Effort to Identify Novel Human Secreted and Transmembrane Proteins:
 A Bioinformatics Assessment
 JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
 PUBMED 12975309
 REFERENCE 2 (bases 1 to 2598)
 Clark, H.F.
 TITLE Direct Submission
 JOURNAL Submitted (01-ANG-2003) Department of Bioinformatics, Genentech,
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA
 FEATURES
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 ORIGIN
 Query Match 100.0%; Score 468; DB 8; Length 2598;
 Best Local Similarity 100.0%; Pred. No. 1.8e-107;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCTCTGAGTGGGCGCTGTGCTTCGGAATGAAGACTGGCAATGAAGCTGCTTAT 60
 DB 67 ATGCTCTGAGTGGGCGCTGTGCTTCGGAATGAAGACTGGCAATGAAGCTGCTTAT 126

QY 61 CTGCATATAACAGCTTCTAGCTGAGAGGCTGATGACAGGAAAGTCAATTAAGTGAA 120
 DB 127 CTGCATATAACAGCTTCTAGCTGAGAGGCTGATGACAGGAAAGTCAATTAAGTGAA 186
 QY 121 GAGATCAGCTGTGTCCTCCCAATGAGTGTGCTGAGTCCAGCTGTGTCCTGCTGAGT 180
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 DB 427 CTGTGACAGGCTGCTGAAGCCGATCAGCTTCAGACTCAGCTTCAGCTTCAGCTTCAGCTTC 486
 QY 421 GCGTGAATGCCCCCATCAGACTTCTACTTCCAGAGCTGTACTAG 468
 DB 487 GCGTGAATGCCCCCATCAGACTTCTACTTCCAGAGCTGTACTAG 534
 RESULT 18
 HSA242738
 LOCUS HSA242738 2604 bp mRNA linear PRI 15-APR-2005
 DEFINITION Homo sapiens mRNA for interleukin-1-like protein 1 (IL1L1 gene)
 transcribed 2.
 ACCESSION AJ242738
 VERSION AJ242738.1 GI:6165335
 KEYWORDS IL1L1 gene; interleukin-1-like protein 1.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE 1
 Barton, J.L., Herbst, R., Bosio, D., Higgins, L., and Nicklin, M.J.
 A tissue specific IL-1 receptor antagonist homolog from the IL-1
 cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities
 Eur. J. Immunol. 30 (11), 3299-3308 (2000)
 JOURNAL 11093146
 REFERENCE 2 (bases 1 to 2604)
 Nicklin, M.J.
 TITLE Direct Submission
 JOURNAL Submitted (09-JUN-1992) Nicklin M.J., Division of Molecular and
 Genetic Medicine, University of Sheffield, Royal Hallamshire
 Hospital, Glossop Road, Sheffield, S10 2JF, UNITED KINGDOM
 FEATURES
 source
 1. 2604
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 73. 540
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LOCUS BD211435 2648 bp DNA linear PAT 17-JUL-2003
 DEFINITION A novel interleukin-1 receptor antagonist and uses thereof.
 ACCESSION BD211435
 VERSION BD211435.1 GI:33021205
 KEYWORDS JP 2002510492-A/4.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 2648)
 REFERENCE Ford J. and Pace A.
 AUTHORS A novel interleukin-1 receptor antagonist and uses thereof
 JOURNAL Patent: JP 2002510492-A 4 09-APR-2002;
 COMMENT HYSEO INC
 OS Homo sapiens (human)
 PN JP 2002510492-A/4
 PD 09-APR-2002
 PF 05-APR-1999 JP 2000542457
 PR 03-APR-1998 US 09/055010,15-MAY-1998 US 09/079909 PR
 20-JUL-1998 US 09/082364,19-JUN-1998 US 09/099818 PR
 31-JUL-1998 US 09/127698,13-JAN-1999 US 09/229591 PR
 11-FEB-1999 US 09/251370
 PI JOHN FORD, ANN PACE
 PC C12N15/09,A61K38/00,C07K14/52,C07K14/545,C07K16/24,C12N1/15,
 PC C12N1/19,
 PC C12N1/21,C12N5/10,C12Q1/68,G01N33/50,G01N33/566,G01N33/68, PC
 C12N15/00,
 PC A61K37/02,C12N5/00
 CC A novel interleukin-1 receptor antagonist and uses thereof FH
 KEY Location/Qualifiers
 FT source 1..2648
 FT Location/Qualifiers
 1..2648
 /organism='Homo sapiens (human)'.
 /molecule='genomic DNA'
 /db_xref='taxon:9606'
 ORIGIN
 Query Match 100.0%; Score 468; DB 6; Length 2648;
 Best Local Similarity 100.0%; Pred. No. 1.8e-107;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGAGCTCGGATGGAAGTCTTTAT 60
 Db 62 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGAGCTCGGATGGAAGTCTTTAT 121
 Oy 61 CTGCATATAACACAGCTTTAGCTGAGAGGCTGCATCAGGGAAGTCAATTAAGTGAA 120
 Db 122 CTGCATATAACACAGCTTTAGCTGAGAGGCTGCATCAGGGAAGTCAATTAAGTGAA 181
 Oy 121 GAGATCAGCTGTGCTCCCAATCGGTGGCTGGATGCAAGCTGTCCCGTCACTTGGGT 180
 Db 182 GAGATCAGCTGTGCTCCCAATCGGTGGCTGGATGCAAGCTGTCCCGTCACTTGGGT 241
 Oy 181 GTCCAGAGTGAAGCCAGTCTGTCTATGTGGGGTGGGGGCAAGAGCCGATCTTAACATA 240
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 Oy 241 GAGCCAGTGAACATCATGAGAGCTCTATCTTGTGTCGAAGGAATCAAGAGCTTCACTTC 300
 Db 302 GAGCCAGTGAACATCATGAGAGCTCTATCTTGTGTCGAAGGAATCAAGAGCTTCACTTC 361
 Oy 301 TACCGGGGAGACATGAGGCTTCACTTCAGCTTGGAGTGGCTGCTTCACTTCGAGTTC 360
 Db 362 TACCGGGGAGACATGAGGCTTCACTTCAGCTTGGAGTGGCTGCTTCACTTCGAGTTC 421
 Oy 361 CTGTGACAGGCTGCTGAAGCCGATCAGCTGTGAGATCAACCAAGCTTCCGAGAAATGAT 420
 Db 422 CTGTGACAGGCTGCTGAAGCCGATCAGCTGTGAGATCAACCAAGCTTCCGAGAAATGAT 481
 Oy 421 GGCTGAATGCCCCCATCAGAGCTTCTACTTCCAGAGTGTGACTAG 468

Db 482 GGCTGAATGCCCCCATCAGAGCTTCTACTTCCAGAGTGTGACTAG 529
 RESULT 21
 LOCUS AR181995 2648 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 6 from patent US 6337072.
 ACCESSION AR181995
 VERSION AR181995.1 GI:20224911
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 1 (bases 1 to 2648)
 AUTHORS Ford J. and Pace A.
 JOURNAL Interleukin-1 receptor antagonist and recombinant production
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 SOURCE Location/Qualifiers
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 /molecule='unassigned DNA'
 ORIGIN
 Query Match 100.0%; Score 468; DB 6; Length 2648;
 Best Local Similarity 100.0%; Pred. No. 1.8e-107;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGAGCTCGGATGGAAGTCTTTAT 60
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 Db 242 GTCCAGAGTGAAGCCAGTCTGTCTATGTGGGGTGGGGGCAAGAGCCGATCTTAACATA 301
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 Db 302 GAGCCAGTGAACATCATGAGAGCTCTATCTTGTGTCGAAGGAATCAAGAGCTTCACTTC 361
 Oy 301 TACCGGGGAGACATGAGGCTTCACTTCAGCTTGGAGTGGCTGCTTCACTTCGAGTTC 360
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 Oy 361 CTGTGACAGGCTGCTGAAGCCGATCAGCTGTGAGATCAACCAAGCTTCCGAGAAATGAT 420
 Db 422 CTGTGACAGGCTGCTGAAGCCGATCAGCTGTGAGATCAACCAAGCTTCCGAGAAATGAT 481
 Oy 421 GGCTGAATGCCCCCATCAGAGCTTCTACTTCCAGAGTGTGACTAG 468
 Db 482 GGCTGAATGCCCCCATCAGAGCTTCTACTTCCAGAGTGTGACTAG 529
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 DEFINITION Sequence 6 from patent US 6426191.
 ACCESSION AR221129
 VERSION AR221129.1 GI:23328014
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 1 (bases 1 to 2648)


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Db      302 GAGCAGTGAACATCATGAGACTCTATTTGGTGCAGAGATCCAGAGCTTCACTTC 361
Qy      301 TACCGGCGGAGCATGAGGCTCACTCCAGCTTCCAGTGGGCTTACCGGGGCTGTTG 360
Db      362 TACCGGCGGAGCATGAGGCTCACTCCAGCTTCCAGTGGGCTTACCGGGGCTGTTG 421
Qy      361 CTGTGACGAGTGCCTGAGCCGATCAGCTGTCAAGACTCACCAGCTTCCGAGATGGT 420
Db      422 CTGTGACGAGTGCCTGAGCCGATCAGCTGTCAAGACTCACCAGCTTCCGAGATGGT 481
Qy      421 GGCTGGAATGCCCTCATCAGACTTCTTACTTCCAGCGTGTGACTAG 468
Db      482 GGCTGGAATGCCCTCATCAGACTTCTTACTTCCAGCGTGTGACTAG 529

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RESULT 25
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DEFINITION Homo sapiens interleukin 1 family, member 5 (delta), transcript
            variant 2, mRNA (cDNA clone MGC:29840 IMAGE:4996939), complete cds.
ACCESSION BC024747
VERSION   BC024747.1  GI:19353229
KEYWORDS  MGC.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homiidae; Homo
          1 (bases 1 to 2692)
          Strauberg, R.L., Felngold, E.A., Grouse, L.H., Derge, J.G.,
          Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
          Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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          Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
          Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
          Scheetz, T.E., Brownstein, M.J., Udell, T.B., Toshiyuki, S.,
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          Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
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          Wooley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
          Vallat, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
          Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
          Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
          Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
          Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmeitz, J., Myers, R.M.,
          Butcher, F.D., Schein, J.E., Jones, S.J., Skalska, U., Marra, M.A.,
          Schmeitz, A., Schein, J.E., Jones, S.J., Skalska, U., Marra, M.A.,
          Generation and initial analysis of more than 15,000 full-length
          human and mouse cDNA sequences
          Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
          12477932
          2 (bases 1 to 2692)
          Strauberg, R.
          Direct Submission
          Submitted (01-MAR-2002) National Institutes of Health, Mammalian
          Gene Collection (MGC) Cancer Genomics Office, National Cancer
          Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
          USA

```

REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabp-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILML)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.bhsc.bcm.tmc.edu/cdna/>

Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louie, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILML at: <http://image.llnl.gov>
Series: IRAX Plate: 42 Row: K Column: 16
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 27894309.

FEATURES

source

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CDS

ORIGIN

Query Match 100.0%; Score 468; DB 8; Length 2692;
Best Local Similarity 100.0%; Pred. No. 1.8e-107;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 ATGCTCTGAGTGGGGGCTGTGCTCCGATGAAGAGCTCGATGAAGGCTTAT 60
134 ATGCTCTGAGTGGGGGCTGTGCTCCGATGAAGAGCTCGATGAAGGCTTAT 193
61 CTGCATATAACCAAGCTTCTAGCTGAGAGGCTGCATCAGAGAGTCAATTAAGTGA 120
194 CTGCATATAACCAAGCTTCTAGCTGAGAGGCTGCATCAGAGAGTCAATTAAGTGA 253
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254 GAGATCAGCTGTGCTCCCAATCGGTGCTGATCCAGCTGTCCCGCTCATCTGGGT 313
181 GTCCAGGTGAAGCCAGCTGCTGTCATGTCGGGTGGGGGAGCCGACCTTAACCTA 240
314 GTCCAGGTGAAGCCAGCTGCTGTCATGTCGGGTGGGGGAGCCGACCTTAACCTA 373
241 GAGCAGTGAACATCATGAGAGCTTATTTGGTGCAGAGATCCAGAGCTTCACTTC 300
374 GAGCAGTGAACATCATGAGAGCTTATTTGGTGCAGAGATCCAGAGCTTCACTTC 433
301 TACCGGCGGAGCATGAGGCTCACTCCAGCTTCCAGTGGGCTGCTTACCGGGCTGTTG 360
434 TACCGGCGGAGCATGAGGCTCACTCCAGCTTCCAGTGGGCTGCTTACCGGGCTGTTG 493
361 CTGTGACGAGTGCCTGAGCCGATCAGCTGTCAAGACTCACCAGCTTCCGAGATGGT 420
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421 GGCTGGAATGCCCTCATCAGACTTCTTACTTCCAGCGTGTGACTAG 468

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Db 554 GGCTGAGATGCCCATCACAGACTTCTACTTCCAGAGATGTACTAG 601

RESULT 26
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LOCUS Homo sapiens interleukin-1 receptor antagonist homolog (IL1HY1)
DEFINITION mRNA, complete cds.
ACCESSION AF186094
VERSION AF186094.1 GI:6049804
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2720)
AUTHORS Mulero,J.J., Pace,A.M., Nelken,S.T., Loeb,D.B., Correa,T.R., Dmanac,R. and Ford,J.E.
JOURNAL Biochem. Biophys. Res. Commun. 263 (3), 702-706 (1999)
PUBMED 10512743
REFERENCE 2 (bases 1 to 2720)
AUTHORS Mulero,J.J., Pace,A.M., Nelken,S.T., Loeb,D.B., Correa,T.R., Dmanac,R. and Ford,J.E.
JOURNAL Biochem. Biophys. Res. Commun. 263 (3), 702-706 (1999)
PUBMED 10512743
TITLE Submitted (13-SEP-1999) Functional Genomics, HYSRO Inc., 670 Almamor Ave., Sunnyvale, CA 94086, USA
JOURNAL Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.8e-107;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCTCTGAGTGGGGGCTGTGCTCCGAAATGAAGACTGGCAATGAAGTGTCTTAT 60
Db 163 ATGTCTCTGAGTGGGGGCTGTGCTCCGAAATGAAGACTGGCAATGAAGTGTCTTAT 222
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Db 223 CTGCAATATAACCAAGCTTCTAGCTGAGAGGCTGATGACAGAGGAAGTCAATTAAGTGA 282
QY 121 GAGATCAAGCTGTCTCCCAATCGGTGCTGATGACCAAGCTGTCTCCCGTCACTGGGT 180
Db 283 GAGATCAAGCTGTCTCCCAATCGGTGCTGATGACCAAGCTGTCTCCCGTCACTGGGT 342
QY 181 GTCCAGAGTGAAGCAGTGTCTGATGAGGGTGGGGCAGAGCCGACTCTTAACACTA 240
Db 343 GTCCAGAGTGAAGCAGTGTCTGATGAGGGTGGGGCAGAGCCGACTCTTAACACTA 402
QY 241 GAGCAGAGTGAAGCAGTGTCTGATGAGGGTGGGGCAGAGCCGACTCTTAACACTA 300
Db 403 GAGCAGAGTGAAGCAGTGTCTGATGAGGGTGGGGCAGAGCCGACTCTTAACACTA 462
QY 301 TACCGGCGGAGCATGGAGCTCACTCAGCTTCAGTGGGTGCTTACCGGGCTGTTC 360

Db 463 TACCGGCGGAGCATGGAGCTCACTCAGCTTCAGTGGGTGCTTACCGGGCTGTTC 522

QY 361 CTGTGACCGGTGCTGAGAGCGGATTCAGCTGATGACATCCAGCTTCCGAGATGGT 420
Db 523 CTGTGACCGGTGCTGAGAGCGGATTCAGCTGATGACATCCAGCTTCCGAGATGGT 582

QY 421 GGCTGAGATGCCCATCACAGACTTCTACTTCCAGAGATGTACTAG 468
Db 583 GGCTGAGATGCCCATCACAGACTTCTACTTCCAGAGATGTACTAG 630

RESULT 27
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LOCUS Synthetic construct Homo sapiens clone FLH141291.01L interleukin 1
DEFINITION family member 5 (IL1F5) mRNA, partial cds.
ACCESSION AY893100
VERSION AY893100.1 GI:60810164
KEYWORDS Human ORF Project.
SOURCE Synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 468)
AUTHORS Hines,L., Rolfe,A., Jepson,D., Moreira,D., Raphael,J., Kelley,F., Shen,B., Halleck,A., Koudinya,M., Hu,Y., Zuo,D., Taycher,E., Williamson,J. and Labaer,J.
JOURNAL Cloning of human full-length CDS in Creator (TM) recombinational vector system
TITLE Unpublished
JOURNAL 2 (bases 1 to 468)
AUTHORS Hines,L., Rolfe,A., Jepson,D., Moreira,D., Raphael,J., Kelley,F., Shen,B., Halleck,A., Koudinya,M., Hu,Y., Zuo,D., Taycher,E., Williamson,J. and Labaer,J.
JOURNAL Direct Submission
TITLE Submitted (05-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA
COMMENT This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion (TM) cloning system between the SalI and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus reading frame; 'GG' after last codon and before HindIII site to maintain sequence-verified. Each clone is clonally isolated and full-length sequence-verified.
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ORIGIN
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Best Local Similarity 99.8%; Pred. No. 4.7e-107;
Matches 467; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy	1	ATGGCTCTGAGTGGGCGCTGTGCTTCCGAAATGAAGAATCTGGCATTTGAAGGCTTTAT	60
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Oy	61	CTGCATAATTAACAGCTTCTAGCTGGAGGGCTGCATGACGAGGAAGGTCAATTAAGGTGA	120
Db	61	CTGCATAATTAACAGCTTCTAGCTGGAGGGCTGCATGACGAGGAAGGTCAATTAAGGTGA	120
Oy	121	GAGATCAACGAGGTGTCGCCAATCGGTGGCTGAGATGCGACGCTGTCGCCGTCATCTGGGGT	180
Db	121	GAGATCAACGAGGTGTCGCCAATCGGTGGCTGAGATGCGACGCTGTCGCCGTCATCTGGGGT	180
Oy	181	GTCACAGGTTGGAAGCCAGTGCCCTGTGATGTGGGGTGGGCAAGAGCGCATCTTAACACTA	240
Db	181	GTCACAGGTTGGAAGCCAGTGCCCTGTGATGTGGGGTGGGCAAGAGCGCATCTTAACACTA	240
Oy	241	GAGCCAGTGAACATCATGAGAGCTTATCTTTGGTGGCCAAAGAAATCCAAAGAGCTTACACTTC	300
Db	241	GAGCCAGTGAACATCATGAGAGCTTATCTTTGGTGGCCAAAGAAATCCAAAGAGCTTACACTTC	300
Oy	301	TACCGGCGGGACATGAGGGCTCACTTCACAGCTTCGAGTGGGCTGCTAACCCGGGCTGGTTC	360
Db	301	TACCGGCGGGACATGAGGGCTCACTTCACAGCTTCGAGTGGGCTGCTAACCCGGGCTGGTTC	360
Oy	361	CTGTGCACGGTGCCTTGAAAGCCGATCAGCCTGTGACACTACCCAGCTTCCCGAAGATGGT	420
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Oy	421	GGCTGGAATGGCCCATCATCAGACTTTCTAATCTTCACGAGTGTGACTAG	468
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RESULT 28	LOCUS	AX080398	465 bp	DNA	linear	PAT 22-FB5-200
DEFINITION	Sequence 10 from Parent W00105974.					
ACCESSION	AX080398					
VERSION	AX080398.1	GI:13159844				
KEYWORDS						
SOURCE						
ORGANISM	Homo sapiens (human)					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.					
REFERENCE	1					
AUTHORS	Nicklin M. and Barton J.					
TITLE	The IL-11 gene and polypeptide products					
JOURNAL	Patent: WO 0105974-A 10 25-JAN-2001/ Interleukin Genetics, Inc. (US)					
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Best Local Similarity	100.0%; Pred. No. 1.1e-106; Mismatches 0; Indels 0; Gaps 0					
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DB	61 CTGCATAATTAACCACTTCTAGCTGGAGGGCTGCATGCAAGGAAGTCAATTAAGGTGAA	120				
QY	121 GAGATCAGCGTGCTCCCAATGGGTGGCTGGATGCGACGCTGCCCCCGCTCATCTTGGGT	180				
DB	121 GAGATCAGCGTGCTCCCAATGGGTGGCTGGATGCGACGCTGCCCCCGCTCATCTTGGGT	180				

OY	181	GTCACAGGATGGAAAGCAGTGCCTTGTCATGTGGGGTGGGGCACAGA GCCACTCTTAACATA	240
Db	181	GTCCACGGSTGGAAAGCACTGCTGTGTCATGTGGGGTGGGGCAGGAGGCCACTCTTAACA CTA	240
OY	241	GAGCCAGTGAACATCATGAGCTCTATCTTTGGTGCMAAGAAATCCAGAGCTTACCTTC	300
Db	241	GAGCCAGTGAACATCATGAGCTCTATCTTTGGTGCMAAGAAATCCAGAGCTTACCTTC	300
OY	301	TACCGGGCGGAGCATGGGGCTCACTCCACAGCTTCGAGTCGGCTGACCCGGGCTGGTTC	360
Db	301	TACCGGGCGGAGCATGGGGCTCACTCCACAGCTTCGAGTCGGCTGACCCGGGCTGGTTC	360
OY	361	CTGTGTCACAGTGTGCTTGAAAGCCGANTAGCCTGTGCAAGCTCACCCAGCTTCCCGAATGGT	420
Db	361	CTGTGTCACAGTGTGCTTGAAAGCCGANTAGCCTGTGCAAGCTCACCCAGCTTCCCGAATGGT	420
OY	421	GGCTGGAAATGCCCCCATACAGACTTCTACTTCCAGCAGTGTGAC	465
Db	421	GGCTGGAAATGCCCCCATACAGACTTCTACTTCCAGCAGTGTGAC	465

LOCUS	CO722801	2701 bp	DNA	linear	PAT 03-FEB-200
DEFINITION	Sequence 8735 from Patent WO02068579.				
ACCESSION	CO722801				
VERSION	CO722801.1				
KEYWORDS	GI:42283658				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.				
REFERENCE	1 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof Patent: WO 02068579-A (US) 06-SEP-2002;				
JOURNAL	PE Corporation (NY) 8735 location/Qualifiers				
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ORIGIN					
Query Match	97.6%	Score 457;	DB 6;	Length 2701;	
Best Local Similarity	99.8%	Pred. No. 1.1e-104;			
Matches 468;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1	
Db	1 ATGGTCGAGATGGGGGCGCTGCTTCGGAATGAGAGACTGGGCAATTGAAGGTCTTAT 60 162 ATGGCCCTGAGATGGGGGCGCTGCTTCGGAATGAGAGACTGGGCAATTGAAGGTCTTAT 221 				
Qy	61 CTGCATATAATACACAGCTTCTAGCTGAGAGGCTGCATGACGAGGAGTCAATTAAGGTGA 120 				
Db	222 CTGCATATAATACACAGCTTCTAGCTGAGAGGCTGCATGACGAGGAGTCAATTAAGGTGA 281 				
Qy	121 GAGATCAGCGTGTGTCCCATCGATCGGTGCTGATGTCAGCTGTCCCGCTCATCTGGGT 180 				
Db	282 GAGATCAGCGTGTGTCCCATCGATCGGTGCTGATGTCAGCTGTCCCGCTCATCTGGGT 341 				
Qy	181 GTCCAGGTGGAAGCCATGTGCTGCATGTGGGGTGGGCGAGGACCCGACTTAACACTA 240 				
Db	342 GTCCAGGTGGAAGCCATGTGCTGCATGTGGGGTGGGCGAGGACCCGACTTAACACTA 401 				
Qy	241 GAGCCAGTGAACATCATGAGCTCTCATTTGGTGCAGAGATCCAAGACTTCACTTC 300 				
Db	402 GAGCCAGTGAACATCATGAGCTCTCATTTGGTGCAGAGATCCAAGACTTCACTTC 461 				
Qy	301 TACCGGCGGAGCATGGGGCTCACTTCGAGTTCGAGTGGCTGCTACCC-GGGCTGGTT 359 				

Db 462 TACCGGGGACATGAGGCTTACCTCCAGCTTCCAGTGGCTGCTACCCGGGGCTT 521

Qy 360 CTGTGACGAGTGTCTGAAGCCGATCAGCTGTCAAGTCAACCCAGCTTCCGAGATGG 419

Db 522 CTGTGACGAGTGTCTGAAGCCGATCAGCTGTCAAGTCAACCCAGCTTCCGAGATGG 581

Qy 420 TGGCTGGAATGCCCCCATCAAGCTTCTTCCAGAGTGAAGTCTAG 468

Db 582 TGGCTGGAATGCCCCCATCAAGCTTCTTCCAGAGTGAAGTCTAG 630

RESULT 30
AX675571 480 bp DNA linear PAT 27-MAR-2003

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AX675571
Sequence 21 from Patent WO2055704.
AX675571 GI:29333562

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
AUTHORS
TITLE

Padigan, M., Li, L., Zetser, B.D., Casman, S.J., Shenoy, S.,
Szytek, K.A., Zhong, M., Gangoli, E.A., Burgess, C.E., Paturnian, M.,
Verne, C.A., Taylor, S., Tcherny, V.T., Miller, C.E., Guo, X.,
Baldog, F.L., Grose, W.M., Alsbrook, J.P., Gerlach, V.,
Edinger, M.K., Rothenberg, M.E., Ellerman, K., MacDougall, J.,
Malvankar, U., Millet, I., Peyman, J., Smithson, G., Gunther, E. and
Stone, D.J.
Proteins, polynucleotides encoding them and methods of using the
same
Patent: WO 02055704-A 21 18-JUL-2002;
Curagen Corporation (US)
Location/Qualifiers
1. 480
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

FEATURES
source

ORIGIN

Query Match 75.7%; Score 354.4; DB 6; Length 480;
Best Local Similarity 85.9%; Pred. No. 9.6e-79;
Matches 407; Conservative 0; Mismatches 61; Indels 6; Gaps 1;

Qy 1 ATGCTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTCGCATTTGAAGTCTTTAT 60

Db 1 ATGCTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTCGCATTTGAAGTCTTTAT 60

Qy 61 CTGATATTAATCAACGCTTTCTGCTGAGAGGCTGCATGACGAGAAAGTTCATTAAGTGA 120

Db 61 CTGATATTAATCAACGCTTTCTGCTGAGAGGCTGCATGACGAGAAAGTTCCTCTAGAG 120

Qy 121 GAGATCAGCGTGTGCTCCCAATCGGTGAGTGCAGACCTGTCCCGCTCATCTGGGT 180

Db 121 AAGATCTGATCTTCTTCAAGAGGCTTGGCCCGACCAAGTCTCCCATTTTCTGGGG 180

Qy 181 GTCCAGGCTGAGACCAAGTCTGTCTATGTGGGGTGGGGCAGAGCCGATCTTAAC- 238

Db 181 ATCCAGGAGGAGACCGCTGCTGCTGAGATGTGGAGACAGAAAGGGGCTTCCCTACAG 240

Qy 239 - - - - - TAGAGCCAGTGAACATCATGAGTCTATCTTGTGTCAGAGAAATCAAGCTTC 294

Db 241 CTGAGCAGCCAGTGAACATCATGAGTCTATCTTGTGTCAGAGAAATCAAGAGCTTC 300

Qy 295 ACCTTTACCGGCGGAGACATGAGGCTCACTTCAGACTTCAGAGTGGCTGCTTACCGGGC 354

Db 301 ACCTTTACCGGCGGAGACATGAGGCTCACTTCAGACTTCAGAGTGGCTGCTTACCGGGC 360

Qy 355 TGGTCTCTGTGACAGGTGCTGGAAGCCGATCAGCTGTCAAGTCAACCCAGCTTCCGAG 414

Db 361 TGGTCTCTGTGACAGGTGCTGGAAGCCGATCAGCTGTCAAGTCAACCCAGCTTCCGAG 420

Qy 415 AATGTGCTGGAATGCCCATCAAGACTTTACTTCCAGAGTGTGACTAG 468

Db 421 AATGTGCTGGAATGCCCATCAAGACTTTACTTCCAGAGTGTGACTAG 474

RESULT 31
AX069335 468 bp DNA linear PAT 25-JAN-2001

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AX069335
Sequence 32 from Patent WO0102571.
AX069335 GI:12579200

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE

Rod, J. and Pace, A.
A interleukin-1 receptor antagonist and uses thereof
Patent: WO 0102571-A 32 11-JAN-2001;
HYSEQ, INC. (US)
Location/Qualifiers
1. 468
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

FEATURES
source

ORIGIN

Query Match 75.0%; Score 351.2; DB 6; Length 468;
Best Local Similarity 84.4%; Pred. No. 6.2e-78;
Matches 395; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 1 ATGCTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTCGCATTTGAAGTCTTTAT 60

Db 1 ATGCTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTCGCATTTGAAGTCTTTAT 60

Qy 61 CTGATATTAATCAACGCTTTCTGCTGAGAGGCTGCATGACGAGAAAGTTCATTAAGTGA 120

Db 61 CTGATATTAATCAACGCTTTCTGCTGAGAGGCTGCATGACGAGAAAGTTCATTAAGTGA 120

Qy 121 GAGATCAGCGTGTGCTCCCAATCGGTGAGTGCAGACCTGTCCCGCTCATCTGGGT 180

Db 121 GAGATCAGTGTGCTCCCAATCGGTGAGTGCAGACCTGTCCCGCTCATCTGGGT 180

Qy 181 GTCCAGGCTGGAAGCCAGTCTGTCTATGTGGGGTGGGGCAGAGCCGATCTTAACCTA 240

Db 181 GTTCAAGAGGAGAGCCAGTCTGTCTATGTGGGACAGAGAAAGGGCCAAATCTGAACCTT 240

Qy 241 GAGCCAGTGAACATCATGAGTCTTATCTTGTGTCAGAGAAATCAAGAGCTTCACCTTC 300

Db 241 GAGCCAGTGAACATCATGAGTCTTATCTTGTGTCAGAGAAATCAAGAGCTTCACCTTC 300

Qy 301 TACCGGCGGAGACATGAGGCTCACTTCAGACTTCAGAGTGGCTGCTTACCGGGCTGTTTC 360

Db 301 TACCGGCGGAGATGAGGCTCACTTCAGACTTCAGAGTGGCTGCTTACCGGGCTGTTTC 360

Qy 361 CTGTGACGAGTGTGCTCCCAATCGGTGAGTGCAGACTCAACCCAGCTTCCGAGAAAGT 420

Db 361 CTGTGACACTCAACCGGAAAGTGAACAGCTGTGAGCTCACTCAAGTCTTCCGAGAGCCC 420

Qy 421 GCGTGAATGCCCATCAAGACTTACTTCCAGAGTGTGACTAG 468

Db 421 GCGTGAATGCCCATCAAGACTTACTTCCAGAGTGTGACTAG 468

RESULT 32
AF230378 471 bp mRNA linear ROD 01-NOV-2001

LOCUS
DEFINITION
ACCESSION

AF230378
Mus musculus interleukin-1 delta mRNA, complete cds.

VERSION AF230378.1 GI:9651790
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 471)
 AUTHORS Debetz, R., Timans, J.C., Homey, B., Zurawski, S., Sana, T.R., Lo, S., Wagner, J., Edwards, G., Clifford, T., Menon, S., Bazan, J.F. and Kastelein, R.A.
 TITLE Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function as an antagonist and agonist of NF-kappa B activation through the orphan IL-1 receptor-related protein 2
 JOURNAL J. Immunol. 167 (3), 1440-1446 (2001)
 PUBMED 11466363
 REFERENCE 2 (bases 1 to 471)
 AUTHORS Kastelein, R.A., Timans, J.C., Sana, T., Debetz, R. and Bazan, F.
 TITLE Direct Submission
 JOURNAL Submitted (01-FEB-2000) Molecular Biology, DNAX Research Institute, 901 California Avenue, Palo Alto, CA 94304, USA
 FEATURES
 source Location/Qualifiers
 1..471
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 1..473
 /note="IL-1delta; cytokine"
 /codon_start=1
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 /protein_id="AA091275.1"
 /db_xref="GI:9651791"
 /translation="MNVLSGALCRMKDSALKVYLHNNQLAGLHAERYIKGEISV
 VPRNADLASIPVILGVGGSGQSLCTEKGPIKLPVIMELYLAKSKSFTFY
 RDMGLTSSPESAAVPGWFLCTSPBADQPVRLTQIPDPAMDAPITDVFQCCD"
 ORIGIN
 Query Match 75.0%; Score 351.2; DB 9; Length 471;
 Best Local Similarity 84.4%; Pred. No. 6.2e-78;
 Matches 395; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 QY 1 ATGGCTCTGAGTGGGGGCTGTGCTCCGATGAAGAGCTCGCATTAAGTCTTAT 60
 DB 4 ATGGCTCTGAGTGGGGGCTGTGCTCCGATGAAGAGCTCGCATTAAGTCTTAT 63
 QY 61 CTGCATTAATAACAGCTTCTAGCTGAGAGGCTGCATGCAAGGATCAATTAAGTGA 120
 DB 64 CTGCATTAATAACAGCTTCTAGCTGAGAGGCTGCATGCAAGGATCAATTAAGTGA 123
 QY 121 GAGATCAGCTGTGCTCCCAATCGGTGCTGATGCCAGCTGTCCCGTCATCTGGGT 180
 DB 124 GAGATCAGCTGTGCTCCCAATCGGTGCTGATGCCAGCTGTCCCGTCATCTGGGT 183
 QY 181 GTCCAGAGTGAAGCCAGTGGCTGTCAATGTGGGGTGGGGCAGAGCCGACTTAACA 240
 DB 184 GTCCAGAGTGAAGCCAGTGGCTGTCAATGTGGGGTGGGGCAGAGCCGACTTAACA 243
 QY 241 GAGCAGTGAACATCATGAGCTCTATCTTGCTCCAGGAATCAAGAGCTTCACTTC 300
 DB 244 GAGCAGTGAACATCATGAGCTCTATCTTGCTCCAGGAATCAAGAGCTTCACTTC 303
 QY 301 TACCGGGGAGACATGAGGCTCACTCAAGTTCGCTGCTACCGGGGTGCTTC 360
 DB 304 TACCGGGGAGACATGAGGCTCACTCAAGTTCGCTGCTACCGGGGTGCTTC 363
 QY 361 CTGTGACAGGTGCTGAGAGCCGATCAGCTGTGACAGCTCAACCGAGCTCCGAGATGT 420
 DB 364 CTGTGACAGGTGCTGAGAGCCGATCAGCTGTGACAGCTCAACCGAGCTCCGAGATGT 423
 QY 421 GGCTGATGCCCCCATACAGACTTCTACTTCCAGAGTGTGACTAG 468
 DB 424 GGCTGATGCCCCCATACAGACTTCTACTTCCAGAGTGTGACTAG 471

RESULT 33
 AF200495 1283 bp mRNA linear ROD 11-MAR-2000
 LOCUS Mus musculus interleukin-1 homolog 3 mRNA, complete cds.
 DEFINITION AF200495
 ACCESSION AF200495
 VERSION AF200495.1 GI:7769117
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1283)
 AUTHORS Kumar, S., McDonnell, P.C., Lehr, R., Tierney, L., Timans, M.N., Griswold, D.E., Capper, E.A., Tal-Singer, R., Wells, G.I., Doyle, M.L. and Young, P.R.
 TITLE Identification and initial characterization of four novel members of the interleukin-1 family
 JOURNAL J. Biol. Chem. 275 (14), 10308-10314 (2000)
 PUBMED 10744718
 REFERENCE 2 (bases 1 to 1283)
 AUTHORS Kumar, S., McDonnell, P.C. and Young, P.R.
 TITLE Direct Submission
 JOURNAL Submitted (01-NOV-1999) Bone and Cartilage Biology, UM 2109, Smithline Beecham Pharmaceuticals, 709 Swedeland Rd., King of Prussia, PA 19406, USA
 FEATURES
 source Location/Qualifiers
 1..1283
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /dev_stage="19.5 day embryo"
 110..577
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 /codon_start=1
 /product="interleukin-1 homolog 3"
 /protein_id="AA09251.1"
 /db_xref="GI:7769118"
 /translation="MNVLSGALCRMKDSALKVYLHNNQLAGLHAERYIKGEISV
 VPRNADLASIPVILGVGGSGQSLCTEKGPIKLPVIMELYLAKSKSFTFY
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 ORIGIN
 Query Match 75.0%; Score 351.2; DB 9; Length 1283;
 Best Local Similarity 84.4%; Pred. No. 6e-78;
 Matches 395; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 QY 1 ATGGCTCTGAGTGGGGGCTGTGCTCCGATGAAGAGCTCGCATTAAGTCTTAT 60
 DB 110 ATGGCTCTGAGTGGGGGCTGTGCTCCGATGAAGAGCTCGCATTAAGTCTTAT 169
 QY 61 CTGCATTAATAACAGCTTCTAGCTGAGAGGCTGCATGCAAGGATCAATTAAGTGA 120
 DB 170 CTGCATTAATAACAGCTTCTAGCTGAGAGGCTGCATGCAAGGATCAATTAAGTGA 229
 QY 171 GTCCAGAGTGAAGCCAGTGGCTGTCAATGTGGGGTGGGGCAGAGCCGACTTAACA 240
 DB 230 GTCCAGAGTGAAGCCAGTGGCTGTCAATGTGGGGTGGGGCAGAGCCGACTTAACA 289
 QY 241 GAGCAGTGAACATCATGAGCTCTATCTTGCTCCAGGAATCAAGAGCTTCACTTC 300
 DB 290 GTCCAGAGTGAAGCCAGTGGCTGTCAATGTGGGGTGGGGCAGAGCCGACTTAACA 349
 QY 301 TACCGGGGAGACATGAGGCTCACTCAAGTTCGCTGCTACCGGGGTGCTTC 360
 DB 350 GAGCAGTGAACATCATGAGCTCTATCTTGCTCCAGGAATCAAGAGCTTCACTTC 409
 QY 301 TACCGGGGAGACATGAGGCTCACTCAAGTTCGCTGCTACCGGGGTGCTTC 360
 DB 410 TACCGGGGAGACATGAGGCTCTTACTTCCAGCTTGAATCCGCTGCTACCGAGCTGCTTC 469

Qy 36 CTGTGACGGGTGCTTAAGCCGATAGAGCTGTCAAGTACCCAGCTTCCGAATAGT 420
Db 470 CTGTGACCTCAACGGAGCTGACAGCTGTCAAGTCACTGATCTCGAGACCC 529
Qy 421 GGCTGAGATGCCCCATCAAGACTTCTACTTCCAGCATGTGACTAG 468
Db 530 GCCGTGGATGCTCCATCAAGACTTCTTACGAGGTGACTAG 577

RESULT 34			
AX080392			
LOCUS	AX080392	1284 bp	DNA
DEFINITION	Sequence 4 from Patent WO0105574.		linear PAT 22-FEB-2001

KEYWORDS	SOURCE	ORGANISM	VERSION
	Mus sp.		AA080322.1
	Mus sp.		01.10.2007

REFERENCE
AUTHORS
TITLE
JOURNAL

1
Nicklin, M. and Barton, J.
The il-11 gene and polypeptide products
Parent: WO 0105974-A 4 25-JUN(2001);
Inventor: Nicklin, M. Barton, J.

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source
1. .1284
/organism="Mus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10095"
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Query Match	75.0%	Score 351.2	DB 6	Length 1284
Best Local Similarity	84.4%	Pred. No. 6e-78		
Matches 395	Conservative	0	Mismatches 73	Indels 0
				Gaps 0

Oy	1	TTGGCCCTGAGTGGGGGCGCTGGTGCCTTCGGAATGAAAGAACTCGGACTTGAAGGTGCTTAT	60
Db	113	ATGGTCTTGAATGGGGGCACTATAGCTTCCGATGGAAGAAATTACAGCTTGAAAGTACTGTA	172
Oy	61	CTGCATAATTAACCAAGCTTCTAGCTGGAAGGGCTGATGCAAGGAGAGTCAATTAAGGTGA	120
Db	173	CTGCACAAATTAACCAAGCTGCTGGCTGGAAGGACTGCACAGCAGAGAAAGTCAATTAAGGTGAG	232
Oy	121	GAGATCAAGCTGGTATCCCAATGGGTGGCTGGATGTCAGGCTTGTCCCGCTCATCTCTGGGT	180
Db	233	GAGATCAAGTGTGTTCTCCAAATGGGCACTGAAATGCAAGTCTGTCCCTGTCAATCTGGGGC	292
Oy	181	GTCACAGGTGGAAGCCAGTGCCTGTCAATGGGGGATGGGGCAAGAGCCGACTTAACACTA	240
Db	293	GTTCAAGAGAGAAAGCAAGTGCTTATCTTGTGGGACAGAAAGGGCAATTGTAAGACTT	352
Oy	241	GAGCCAGTGAACATCATGTAGGCTCTATCTTGGTGCCMAAGAAATCCAAGGCTTCACTTTC	300
Db	353	GAGCCAGTGAACATCATGTAGGCTCTTACCTCGGGGGCCAAAGAAATCAAAAGGCTTCACTTTC	412
Oy	361	TACCGGCGGGGACATGGGGGCTCACTCCAGCTTCGATGGGCTGCAGTACCCGGGACTGGTTC	360
Db	413	TACCGGCGGGGATATGGGATTTTAACTTCAGCTTCGAAATCCGCTGGCTTAACCCAGGCTGGTTC	472
Oy	361	CTGTGCAAGGTGCTTGAAAGCCGATCAAGCTGTCAAGCTTCACCCAGCTTCCGAGAAATGGT	420
Db	473	CTGTGCACTCAACCGGAAGCTGACCAAGCCTGTCAAGGCTCACTCAAGATCCCTGAGAGACCC	532
Oy	421	GGCTGGAAATGCCCATCAACAAGCTTTTACTTCCAGCAAGTGTGACTGAG	468
Db	533	GGCTGGAAATGCCCATCAACAAGCTTTTACTTCCAGCAAGTGTGACTGAG	580

RESULT 35
MMU250429
LOCUS

MMU250429	1284 bp	mRNA	linear	ROD 18-APR-2002
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DEFINITION	Mus musculus mRNA for IL-1L1 protein.
ACCESSION	AJ250429
VERSION	AJ250429.1 GI:6165412
KEYWORDS	IL-1L1 protein.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

REFERENCE	AUTHORS	TITLE
1	Barton, J. L., Herbert, R., Bosio, D., Higgins, L. and Nicklin, M. J.	A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities

TITLE	Direct Submission
JOURNAL	Submitted (15-OCT-1999) Nicklin M.J.H., Division of Molecular Genetic Medicine, University of Sheffield, Royal Hallamshire Hospital, Sheffield, S10 2JF, UNITED KINGDOM
COMMENT	Related sequence: A1391190.
FEATURES	Location/Qualifiers

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/organism="Mus musculus"
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/clone="IMAGE 332733"
CDS
113..580

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ORIGIN
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      /translation="MTVSGALCFMRKDSALKVYLHNHQLAGLIAHKYIKGEISIV
      VPRRLDASLSPVLIGVGGSGGSCCTEGKPIKLEPPNIMELIAKSKSKPTFR
      RDMGLTISFESALYPGWFLCTSPADQPVRLTQIPEDPANDAPITDPTFOQC"

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Query Match	Similarity	75.0%	Score 351.2	DB 9	Length 1284
Best Local	84.4%	Pred. No. 6e-78			
Matches 395	Conservative 0	Mismatches 73	Indels 0	Gaps 0	
QY	1	ATGGTCTCGAATGGGGCGCTGTGCTTCCGAATGAAGACTCGACATTGAAGTCTTTAT	60		
Db	113	ATGGTCTCGAATGGGGCGACTATGCTTCGAATGAAGATTACGCTTGAAGTACTGTAT	172		
QY	61	CTGCATAATTAACCAAGCTTTTAACTGAGAGGGCTGCATGACGGAAAGTCAATTAAGGTGA	120		
Db	173	CTGCACATAATCAACGCTGTGCTGGCTGAGAGACATGCACCAAGAAAGTCAATTAAGGTGAG	232		
QY	121	GAGATCAAGCGTGTGCTCCCAATCGGTGGCTGGATGCCAGCTGTCCCGCTATCTGGGT	180		
Db	233	GAGATCAAGTGTGTCTCCAAATCGGGCACTGGATGCCAGTGTGTCCCGTATCTTGGGC	292		
QY	181	GTCAGAGGTGAAAGCCAGTGCCTGTATGTGTGGGTGGGGCAGAGCCGACTTAACTA	240		
Db	293	GTTCAAGGAGAGAACCCAGTGCCTTCTTGTGTGGGCAAGAGAAAGGGCCAAATTTGAAACTT	352		
QY	241	GAGCAGTGAACATCATGAGAGCTCTATCTTGTGTGTCACCAAGAAATCAAGAGCTTACCTTC	300		
Db	353	GAGCAGTGAACATCATGAGCTTACTCGGGGCCAAGAAATCAAGAAAGCTTCACTTC	412		
QY	301	TACCGGGGGGACATGGGGCTCACTCTCAAGCTTGAAGTGGGCTGCTTACCGGGGCTGTTC	360		
Db	413	TACCGGGGGGATATGGGTCTTCACTCTCAAGCTTCCAATTCGCTGCTTACCGAGGCTGGTTC	472		
QY	361	CTGTGACACGGTCTGAAAGCCGATCAAGCTGTGACAGTCAACCCAGCTTCCGAGAAATG	420		
Db	473	CTGTGACCTTACCGGAAGCTGACACAGCTGTTCAGGCTCACTTCAGATCCTTGAGGACCC	532		
QY	421	GAGTGAATGCCCCCATCAAGACTTCACTTCCAGACAGTGAAGTGA	468		

Db 533 GCCTGGATGCTCCATCAGACTTCTACTTTCAGCAGTGTACTAG 580

RESULT 36
LOCUS BD263575 1385 bp DNA linear PAT 17-JUL-2003
DEFINITION IL-1 related polypeptides.
ACCESSION BD263575
VERSION BD263575.1 GI:33073343
KEYWORDS JP 200253122-A/9.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Goddard, A. and Pan, J.
TITLE IL-1 related polypeptides
JOURNAL Patent: JP 200253122-A 9 08-OCT-2002;
GENENTECH INC
COMMENT OS Mus musculus (mouse)
PN JP 200253122-A/9
PD 08-OCT-2002
PF 22-DEC-1999 JP 2000591188
PR 23-DEC-1998 US 60/113430, 22-JAN-1999 US 60/116843 PR
PI AUDREY GODDARD, JAMES PAN
PC C12N15/09, C07K14/475, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC C12N5/10,
CC C12P21/02, C12P21/08, C12N15/00, C12N5/00
CDS IL-1 related polypeptides
FH Key Location/Qualifiers
FT source 1..1385
Location/Qualifiers
1..1385
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/mol_type="genomic DNA"
/db_xref="taxon:10090"

ORIGIN
Query Match 75.0%; Score 351.2; DB 6; Length 1385;
Best Local Similarity 84.4%; Pred. No. 66-78;
Matches 395; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 1 ATGGCTCTGAGTGGGGGCTGTGCTTCCGATGAAGACTCGCATTAAGTCTTTAT 60
DB 145 ATGGTTCTGAGTGGGGGCACTATGCTTCCGATGAAGATTCAGCTTGAAGTACTGTAT 204
QY 61 CTGCTAATAACCAAGCTTCTAGCTGAGAGGCTGATGAGGAAAGTCAATTAAGTGAA 120
DB 205 CTGCACATAAACAAGCTGCTGCTGAGAGACTGCACCAAGAGATTAAGAGTGAG 264
QY 121 GAGATCAGCTGTGCCCCCAATCGGTGCTGATGAGCCGCTGCCCCGTCATCTGGGT 180
DB 265 GAGATCAGTGTGCTCCAAATCGGGCACTGATGCTGCTGCTGCTGCTGCTGCTGCTG 324
QY 181 GTCCAGGCTGAAGCCAGTGCCTGTCAATGTGGGGTGGGGCAGAGCCGACTTAACTA 240
DB 325 GTTCAAGAGAGAGGCGAGTGCCTATCTGTGGGACAAGAAAGGGCCAATTTGAACTT 384
QY 241 GAGCCAGTGAACATCATGAGCTTATCTTGTGTGTCAGAGAAATCAAGAGCTTCACTTC 300
DB 385 GAGCCAGTGAACATCATGAGCTTACCTCGGGGCCAAGAAATCAAGAGCTTCACTTC 444
QY 301 TACCGGGGAGCATGGGGCTCACTCGAGCTTGAAGTGGGCTGCTACCGGGGCTGTTTC 360
DB 445 TACCGGGGAGATATGGGTCTTACCTCAAGCTTGAATCGGTGCTTACCGGGGCTGTTTC 504
QY 361 CTGTGACGAGTGCCTGAAGCCGATCAGCTGTCAAGACTCAACCAAGCTTCCGAGAAATGT 420
DB 505 CTGTGACCTTCACCGGAAAGCTGACCAAGCTGTCTGAGGCTCACTGATCCCTGAGAGACCC 564

QY 421 GGCTGAATGCCCCATCAGACTTCTACTTCCAGCAGTGTACTAG 468
DB 565 GCCTGGATGCTCCATCAGACTTCTACTTTCAGCAGTGTACTAG 612

RESULT 37
LOCUS BD106430 470 bp DNA linear PAT 18-SEP-2002
DEFINITION Mammalian cytokines; related reagents and methods.
ACCESSION BD106430
VERSION BD106430.1 GI:23201248
KEYWORDS JP 2002501496-A/1.
SOURCE Chlamydia sp.
ORGANISM Chlamydia sp.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.

REFERENCE
AUTHORS Hedrick, J.A., Sana, T.R., Bazan, F. and Kastelein, R.A.
TITLE Mammalian cytokines
JOURNAL Patent: JP 2002501496-A 1 15-JAN-2002;
SCHERING CORP
COMMENT PN JP 2002501496-A/1
PD 15-JAN-2002
PF 17-APR-1998 JP 1998546087
PR 21-APR-1997 US 08/837627, 06-AUG-1997 US 60/055111 PI
PI JOSEPH A HEDRICK, THEODORE R SANA, FERNANDO BAZAN, ROBERT A PI KASTELEIN
PC C07K14/545, C07K14/54, C12P21/02, C12N15/12
CC Strandedness: Single;
CDS Topology: Linear;
FH Key Location/Qualifiers
FT CDS 1..468
Location/Qualifiers
1..470
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/mol_type="genomic DNA"
/db_xref="taxon:35827"

ORIGIN
Query Match 74.8%; Score 350.2; DB 6; Length 470;
Best Local Similarity 84.4%; Pred. No. 1.1e-77;
Matches 394; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 1 ATGGCTCTGAGTGGGGGCTGTGCTTCCGATGAAGACTCGCATTAAGTCTTTAT 60
DB 4 ATGGTTCTGAGTGGGGGCACTATGCTTCCGATGAAGATTCAGCTTGAAGTACTGTAT 63
QY 61 CTGCTAATAACCAAGCTTCTAGCTGAGAGGCTGATGAGGAAAGTCAATTAAGTGAA 120
DB 64 CTGCACATAAACAAGCTGCTGCTGAGAGACTGCACCAAGAGATTAAGAGTGAG 123
QY 121 GAGATCAGCTGTGCCCCCAATCGGTGCTGATGAGCCGCTGCCCCGTCATCTGGGT 180
DB 124 GAGATCAGTGTGCTCCAAATCGGGCACTGATGCTGCTGCTGCTGCTGCTGCTGCTG 183
QY 181 GTCCAGGCTGAAGCCAGTGCCTGTCAATGTGGGGTGGGGCAGAGCCGACTTAACTA 240
DB 184 GTTCAAGAGAGAGGCGAGTGCCTATCTGTGGGACAAGAAAGGGCCAATTTGAACTT 243
QY 241 GAGCCAGTGAACATCATGAGCTTATCTTGTGTGTCAGAGAAATCAAGAGCTTCACTTC 300
DB 244 GAGCCAGTGAACATCATGAGCTTACCTCGGGGCCAAGAAATCAAGAGCTTCACTTC 303
QY 301 TACCGGGGAGCATGGGGCTCACTCGAGCTTGAAGTGGGCTGCTACCGGGGCTGTTTC 360
DB 304 TACCGGGGAGATATGGGTCTTACCTCAAGCTTGAATCCCTGCTACCAAGGCTGTTTC 363
QY 361 CTGTGACGAGTGCCTGAAGCCGATCAGCTGTCAAGACTCAACCAAGCTTCCGAGAAATGT 420
DB 364 CTGTGACCTTCACCGGAAAGCTGACCAAGCTGTCAAGGCTCACTGATCCCTGAGAGACCC 423
QY 421 GGCTGAATGCCCCATCAGACTTCTACTTCCAGCAGTGTACTAG 467

Db 424 GCCTGGGATGCTCCATCAGAGCTTCTACTTTCAGCAGTGTGACTA 470

RESULT 38
AX080399 465 bp DNA linear PAT 22-FEB-2001
LOCUS AX080399
DEFINITION Sequence 11 from Patent WO0105974.
ACCESSION AX080399
VERSION AX080399.1 GI:13159845
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 Nicklin, M. and Barton, J.
The 11-111 gene and polypeptide products
Patent: WO 0105974-A 11-25-JAN-2001;
JOURNAL Interleukin Genetics, Inc. (US)

FEATURES
source location/Qualifiers
1..465
/organism="Mus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10095"

ORIGIN
Query Match 74.4%; Score 348.2; DB 6; Length 465;
Best Local Similarity 84.3%; Pred. No. 3.5e-77;
Matches 392; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 1 ATGGCTCTGAGTGGGGGCTGTGCTTCCGAATGAAGAGCTCGCATTAAGAGTCTTAT 60
Db 1 ATGGCTCTGAGTGGGGGCTGTGCTTCCGAATGAAGAGTCTCGCATTAAGAGTCTTAT 60
QY 61 CTGCATATAACCAAGCTTCTAGCTGAGAGGCTGCATCAAGGAAGTCAATTAAGTGAA 120
Db 61 CTGCATATAACCAAGCTTCTAGCTGAGAGGCTGCATCAAGGAAGTCAATTAAGTGAG 120
QY 121 GAGATCAGCTGTGCTCCCAATCGGTGGCTGAGATCCAGCCTGTCTCCCGTCACTTGGGT 180
Db 121 GAGATCAGCTGTGCTCCCAATCGGTGGCTGAGATCCAGCCTGTCTCCCGTCACTTGGGT 180
QY 121 GAGATCAGCTGTGCTCCCAATCGGTGGCTGAGATCCAGCCTGTCTCCCGTCACTTGGGT 180
Db 121 GAGATCAGCTGTGCTCCCAATCGGTGGCTGAGATCCAGCCTGTCTCCCGTCACTTGGGT 180
QY 181 GTCCAGAGGTGAAGCCAGTGCCTGTCAATGTGGGTGGGGCAGAGCCGACTCTTAACACTA 240
Db 181 GTCCAGAGGTGAAGCCAGTGCCTGTCAATGTGGGTGGGGCAGAGCCGACTCTTAACACTA 240
QY 241 GAGCAGTGAACATCATGAGCTTATCTTGTGTCGCAAGGATCCAAAGAGCTTCACTTC 300
Db 241 GAGCAGTGAACATCATGAGCTTATCTTGTGTCGCAAGGATCCAAAGAGCTTCACTTC 300
QY 301 TACCGGGGGGACATGGGGCTCACTCCAGCTTCAAGTCCGCTGCTTACCCGGGTGCTTC 360
Db 301 TACCGGGGGGACATGGGGCTCACTCCAGCTTCAAGTCCGCTGCTTACCCGGGTGCTTC 360
QY 361 CTGTGACAGGTGCTGAGAGCCGATCAGCTGTGCACTCAAGCTTCCCGAGAAATGAT 420
Db 361 CTGTGACAGGTGCTGAGAGCCGATCAGCTGTGCACTCAAGCTTCCCGAGAAATGAT 420
QY 421 GCGTGAATGCCCCCATCAGAGCTTCTTACCTCCAGCAGTGTGAC 465
Db 421 GCGTGAATGCCCCCATCAGAGCTTCTTACCTCCAGCAGTGTGAC 465

RESULT 39
BD124060 468 bp DNA linear PAT 18-SEP-2002
LOCUS BD124060
DEFINITION DNA and polypeptide of IL-1-delta.
ACCESSION BD124060
VERSION BD124060.1 GI:23219005
KEYWORDS JP 2002500046-A/1.
SOURCE Mus musculus (house mouse)

REFERENCE
AUTHORS Sims, J.R.
TITLE DNA and polypeptide of IL-1-delta
JOURNAL Patent: JP 2002500046-A 1 08-JAN-2002;
IMMUNEX CORP
COMMENT OS Mus musculus (mouse)
PN JP 2002500046-A/1
PD 08-JAN-2002
PR 08-JAN-1999 JP 2000527652
PR 09-JAN-1998 US 60/071074, 01-JUN-1998 US 60/087393 PI
PC C12N15/09, C07K14/545, C07K16/24, C12N1/19, C12N1/21, C12N5/10, PC
C12P21/08//
CC C12M1/00, C12N15/00, C12N5/00
CC DNA and polypeptide of IL-1-delta
FH Key location/Qualifiers
FT source 1..468
FT location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

ORIGIN
Query Match 74.4%; Score 348.2; DB 6; Length 468;
Best Local Similarity 84.3%; Pred. No. 3.5e-77;
Matches 392; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 1 ATGGCTCTGAGTGGGGGCTGTGCTTCCGAATGAAGAGCTCGCATTAAGAGTCTTAT 60
Db 4 ATGGCTCTGAGTGGGGGCTGTGCTTCCGAATGAAGAGTCTCGCATTAAGAGTCTTAT 63
QY 61 CTGCATATAACCAAGCTTCTAGCTGAGAGGCTGCATCAAGGAAGTCAATTAAGTGAA 120
Db 64 CTGCATATAACCAAGCTTCTAGCTGAGAGGCTGCATCAAGGAAGTCAATTAAGTGAG 123
QY 121 GAGATCAGCTGTGCTCCCAATCGGTGGCTGAGATCCAGCCTGTCTCCCGTCACTTGGGT 180
Db 124 GAGATCAGCTGTGCTCCCAATCGGTGGCTGAGATCCAGCCTGTCTCCCGTCACTTGGGT 183
QY 181 GTCCAGAGGTGAAGCCAGTGCCTGTCAATGTGGGTGGGGCAGAGCCGACTCTTAACACTA 240
Db 184 GTCCAGAGGTGAAGCCAGTGCCTGTCAATGTGGGTGGGGCAGAGCCGACTCTTAACACTA 243
QY 241 GAGCAGTGAACATCATGAGCTTATCTTGTGTCGCAAGGATCCAAAGAGCTTCACTTC 300
Db 244 GAGCAGTGAACATCATGAGCTTATCTTGTGTCGCAAGGATCCAAAGAGCTTCACTTC 303
QY 301 TACCGGGGGGACATGGGGCTCACTCCAGCTTCAAGTCCGCTGCTTACCCGGGTGCTTC 360
Db 304 TACCGGGGGGATATGGGTCTTACCTCCAGCTTCAAGTCCGCTGCTTACCCGGGTGCTTC 363
QY 361 CTGTGACAGGTGCTGAGAGCCGATCAGCTGTGCACTCAAGCTTCCCGAGAAATGAT 420
Db 364 CTGTGACAGCTTCAAGAGCCGATCAGCTGTGCACTCAAGCTTCCCGAGAAATGAT 423
QY 421 GCGTGAATGCCCCCATCAGAGCTTCTTACCTCCAGCAGTGTGAC 465
Db 424 GCGTGAATGCCCCCATCAGAGCTTCTTACCTCCAGCAGTGTGAC 468

RESULT 40
BD211432 338 bp DNA linear PAT 17-JUL-2003
LOCUS BD211432
DEFINITION A novel interleukin-1 receptor antagonist and uses thereof.
ACCESSION BD211432
VERSION BD211432.1 GI:33021202
KEYWORDS JP 2002510492-A/1.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 338)
AUTHORS Ford, J. and Pace, A.
TITLE A novel interleukin-1 receptor antagonist and uses thereof
JOURNAL Patent: JP 2002510492-A 1 09-APR-2002;
HYSEQ INC
COMMENT OS Homo sapiens (human)
PN JP 2002510492-A/1
PD 09-APR-2002
PR 05-APR-1999 JP 2000542457
PR 03-APR-1998 US 09/055010, 15-MAY-1998 US 09/079909 PR
20-MAY-1998 US 09/082364, 19-JUN-1998 US 09/099818 PR
31-JUL-1998 US 09/127698, 13-JAN-1999 US 09/229591 PR
1-FEB-1999 US 09/251370
P1 JOHN FORD, ANN PACE
PC C12N15/09, A61K38/00, C07K14/52, C07K14/545, C07K16/24, C12N1/15,
PC C12N1/21, C12N5/10, C12Q1/68, G01N33/50, G01N33/566, G01N33/68, PC
C12N15/00,
PC A61K37/02, C12N5/00
CC A novel interleukin-1 receptor antagonist and uses thereof FH
Key Location/Qualifiers
FT source 1..338
FT /organism='Homo sapiens (human)'.
FEATURES
source 1..338
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
ORIGIN
Query Match 51.9%; Score 243; DB 6; Length 338;
Best Local Similarity 100.0%; Pred. No. 1.4e-50;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 226 CCGACTTAACACTAGAGCCAGTGAACATCATGAGCTCTATCTTGGTCCAGGAATCC 285
DB 1 CCGACTTAACACTAGAGCCAGTGAACATCATGAGCTCTATCTTGGTCCAGGAATCC 60
QY 286 AAGAGCTTCACTTCTACCGCGGAGCATGAGGCTCACTTCAGACTTCGAGTGGCTGCC 345
DB 61 AAGAGCTTCACTTCTACCGCGGAGCATGAGGCTCACTTCAGACTTCGAGTGGCTGCC 120
QY 346 TACCCGGGCTGTTCTCTGTGACGCGTCCGTGAAGCCGATCAGCTGTCAAGTCAACCAG 405
DB 121 TACCCGGGCTGTTCTCTGTGACGCGTCCGTGAAGCCGATCAGCTGTCAAGTCAACCAG 180
QY 406 CTTCCCGAGATGTGCTGGAATGCCCATCAAGACTTCTAATTCCAGAGTGTGAC 465
DB 181 CTTCCCGAGATGTGCTGGAATGCCCATCAAGACTTCTAATTCCAGAGTGTGAC 240
QY 466 TAG 468
DB 241 TAG 243
RESULT 41
ARI81992 357 bp DNA linear PAT 20-APR-2002
LOCUS ARI81992
DEFINITION Sequence 1 from patent US 6337072.
ACCESSION ARI81992
VERSION ARI81992.1 GI:20224908
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 357)
AUTHORS Ford, J. and Pace, A.
TITLE Interleukin-1 receptor antagonist and recombinant production
thereof

JOURNAL Patent: US 6337072-A 1 08-JAN-2002;
FEATURES Location/Qualifiers
source 1..357
/organism='unknown'
/mol_type='unassigned DNA'
ORIGIN
Query Match 51.9%; Score 243; DB 6; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.4e-50;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 226 CCGACTTAACACTAGAGCCAGTGAACATCATGAGCTCTAATCTTGGTCCAGGAATCC 285
DB 1 CCGACTTAACACTAGAGCCAGTGAACATCATGAGCTCTAATCTTGGTCCAGGAATCC 60
QY 286 AAGAGCTTCACTTCTACCGCGGAGCATGAGGCTCACTTCAGACTTCGAGTGGCTGCC 345
DB 61 AAGAGCTTCACTTCTACCGCGGAGCATGAGGCTCACTTCAGACTTCGAGTGGCTGCC 120
QY 346 TACCCGGGCTGTTCTCTGTGACGCGTCCGTGAAGCCGATCAGCTGTCAAGTCAACCAG 405
DB 121 TACCCGGGCTGTTCTCTGTGACGCGTCCGTGAAGCCGATCAGCTGTCAAGTCAACCAG 180
QY 406 CTTCCCGAGATGTGCTGGAATGCCCATCAAGACTTCTAATTCCAGAGTGTGAC 465
DB 181 CTTCCCGAGATGTGCTGGAATGCCCATCAAGACTTCTAATTCCAGAGTGTGAC 240
QY 466 TAG 468
DB 241 TAG 243

RESULT 42
AR221126 357 bp DNA linear PAT 26-SEP-2002
LOCUS AR221126
DEFINITION Sequence 1 from patent US 6426191.
ACCESSION AR221126
VERSION AR221126.1 GI:23328011
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 357)
AUTHORS Ford, J. and Pace, A.
TITLE Assays involving an IL-1 receptor antagonist
JOURNAL Patent: US 6426191-A 1 30-JUL-2002;
Hyseq, Inc.; Sunnyvale, CA
FEATURES Location/Qualifiers
source 1..357
/organism='unknown'
/mol_type='genomic DNA'
ORIGIN
Query Match 51.9%; Score 243; DB 6; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.4e-50;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 226 CCGACTTAACACTAGAGCCAGTGAACATCATGAGCTCTAATCTTGGTCCAGGAATCC 285
DB 1 CCGACTTAACACTAGAGCCAGTGAACATCATGAGCTCTAATCTTGGTCCAGGAATCC 60
QY 286 AAGAGCTTCACTTCTACCGCGGAGCATGAGGCTCACTTCAGACTTCGAGTGGCTGCC 345
DB 61 AAGAGCTTCACTTCTACCGCGGAGCATGAGGCTCACTTCAGACTTCGAGTGGCTGCC 120
QY 346 TACCCGGGCTGTTCTCTGTGACGCGTCCGTGAAGCCGATCAGCTGTCAAGTCAACCAG 405
DB 121 TACCCGGGCTGTTCTCTGTGACGCGTCCGTGAAGCCGATCAGCTGTCAAGTCAACCAG 180
QY 406 CTTCCCGAGATGTGCTGGAATGCCCATCAAGACTTCTAATTCCAGAGTGTGAC 465
DB 181 CTTCCCGAGATGTGCTGGAATGCCCATCAAGACTTCTAATTCCAGAGTGTGAC 240

QY 466 TAG 468
|||
Db 241 TAG 243

RESULT 43
AR302954
LOCUS AR302954 357 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 1 from patent US 6541623.
ACCESSION AR302954
VERSION AR302954.1 GI:31691554
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
1 (bases 1 to 357)
FORD, J., HO, A.S.Y. and PACE, A.
TITLE Interleukin-1 receptor antagonist and uses thereof
JOURNAL Patent: US 6541623-A 1 01-APR-2003;
Hyseq, Inc.; Sunnyvale, CA

FEATURES
Location/Qualifiers
source 1..357
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 51.9%; Score 243; DB 6; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.4e-50;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 CCGACTTAACACTAGAGCCAGTGAACATCATGAGCTTATCTTGTCACAGAAATCC 285
|||
Db 1 CCGACTTAACACTAGAGCCAGTGAACATCATGAGCTTATCTTGTCACAGAAATCC 60

QY 286 AAGAGCTTACCTTTTACCCGGGAGACATGAGGCTTCACTTCAGCTTTCAGTGGCTGCC 345
|||
Db 61 AAGAGCTTACCTTTTACCCGGGAGACATGAGGCTTCACTTCAGCTTTCAGTGGCTGCC 120

QY 346 TACCCGGGCTGTTCTTCTGTCACGCTGCAAGCCATCAGCTTCAGACTCACCAG 405
|||
Db 121 TACCCGGGCTGTTCTTCTGTCACGCTGCAAGCCATCAGCTTCAGACTCACCAG 180

QY 406 CTTCGCCAGATGCTGCTGGAATGCCCCCATTCACAGACTTCTTCTTCAGAGTGTGAC 465
|||
Db 181 CTTCGCCAGATGCTGCTGGAATGCCCCCATTCACAGACTTCTTCTTCAGAGTGTGAC 240

QY 466 TAG 468
|||
Db 241 TAG 243

RESULT 44
AX069304
LOCUS AX069304 357 bp DNA linear PAT 25-JAN-2001
DEFINITION Sequence 1 from Patent WO0102571.
ACCESSION AX069304
VERSION AX069304.1 GI:12579176
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
1
FORD, J. and PACE, A.
TITLE A interleukin-1 receptor antagonist and uses thereof
JOURNAL Patent: WO 0102571-A 1 11-JAN-2001;
HYSEQ, INC. (US)

FEATURES
Location/Qualifiers
source 1..357
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

misc_feature 1..357
/note="n = A,T,C or G"

ORIGIN

Query Match 51.9%; Score 243; DB 6; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.4e-50;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 CCGACTTAACACTAGAGCCAGTGAACATCATGAGCTTATCTTGTCACAGAAATCC 285
|||
Db 1 CCGACTTAACACTAGAGCCAGTGAACATCATGAGCTTATCTTGTCACAGAAATCC 60

QY 286 AAGAGCTTACCTTTTACCCGGGAGACATGAGGCTTCACTTCAGCTTTCAGTGGCTGCC 345
|||
Db 61 AAGAGCTTACCTTTTACCCGGGAGACATGAGGCTTCACTTCAGCTTTCAGTGGCTGCC 120

QY 346 TACCCGGGCTGTTCTTCTGTCACGCTGCAAGCCATCAGCTTCAGACTCACCAG 405
|||
Db 121 TACCCGGGCTGTTCTTCTGTCACGCTGCAAGCCATCAGCTTCAGACTCACCAG 180

QY 406 CTTCGCCAGATGCTGCTGGAATGCCCCCATTCACAGACTTCTTCTTCAGAGTGTGAC 465
|||
Db 181 CTTCGCCAGATGCTGCTGGAATGCCCCCATTCACAGACTTCTTCTTCAGAGTGTGAC 240

QY 466 TAG 468
|||
Db 241 TAG 243

RESULT 45
BD211433
LOCUS BD211433 985 bp DNA linear PAT 17-JUL-2003
DEFINITION A novel interleukin-1 receptor antagonist and uses thereof.
ACCESSION BD211433
VERSION BD211433.1 GI:33021203
KEYWORDS JP 2002510492-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
1 (bases 1 to 985)
FORD, J. and PACE, A.
TITLE A novel interleukin-1 receptor antagonist and uses thereof
JOURNAL Patent: JP 2002510492-A 2 09-APR-2002;
HYSEQ INC

COMMENT
OS Homo sapiens (human)
PN JP 2002510492-A/2
PD 09-APR-2002
PF 05-APR-1999 JP 2000542457
PR 03-APR-1998 US 09/055010,15-MAY-1998 US 09/079909 PR
20-MAY-1998 US 09/082364,19-JUN-1998 US 09/099818 PR
31-JUL-1998 US 09/127698,13-JAN-1999 US 09/229591 PR
17-FEB-1999 US 09/251370
PI JOHN FORD, ANN PACE
PC C12N15/09, A61K38/00, C07K14/52, C07K14/545, C07K16/24, C12N1/15,
PC C12N1/19,
PC C12N1/21, C12N5/10, C12Q1/68, G01N33/50, G01N33/566, G01N33/68, PC
C12N15/00,
PC A61K37/02, C12N5/00
CC A novel interleukin-1 receptor antagonist and uses thereof FH
Key Location/Qualifiers
FT source 1..985
/organism="Homo sapiens (human)".

FEATURES
Location/Qualifiers
source 1..985
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 51.9%; Score 243; DB 6; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.3e-50;

Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 CCGACTTAACACTAGAGCCAGTGAACATCATGAGCTCTATCTTGGTCCCAAGAAATCC 285
DB 1 CCGACTTAACACTAGAGCCAGTGAACATCATGAGCTCTATCTTGGTCCCAAGAAATCC 60

QY 286 AAGAGCTTCACTTCTACCGGCGGAGCATGAGGCTCACTTCAGCTTCGAGTGGCTGCC 345
DB 61 AAGAGCTTCACTTCTACCGGCGGAGCATGAGGCTCACTTCAGCTTCGAGTGGCTGCC 120

QY 346 TACCCGGGCTGGTTCCTGTGCAAGCGTGCCTGAAGCCGATCAGCTTGCAGCTCAACCAG 405
DB 121 TACCCGGGCTGGTTCCTGTGCAAGCGTGCCTGAAGCCGATCAGCTTGCAGCTCAACCAG 180

QY 406 CTTCGCCGAGATGGTGGCTGGAATGCCCCATCAAGCTTCTTCCAGCAGTGTGAC 465
DB 181 CTTCGCCGAGATGGTGGCTGGAATGCCCCATCAAGCTTCTTCCAGCAGTGTGAC 240

QY 466 TAG 468
DB 241 TAG 243

RESULT 46
AR181993 985 bp DNA linear PAT 20-APR-2002
LOCUS AR181993
DEFINITION Sequence 2 from patent US 6337072.
ACCESSION AR181993
VERSION AR181993.1 GI:20224909
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 985)
AUTHORS Ford, J. and Pace, A.
TITLE Interleukin-1 receptor antagonist and recombinant production thereof
JOURNAL Patent: US 6337072-A 2 08-JAN-2002;
FEATURES
source Location/Qualifiers
1..985
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 51.9%; Score 243; DB 6; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.3e-50;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 CCGACTTAACACTAGAGCCAGTGAACATCATGAGCTCTATCTTGGTCCCAAGAAATCC 285
DB 1 CCGACTTAACACTAGAGCCAGTGAACATCATGAGCTCTATCTTGGTCCCAAGAAATCC 60

QY 286 AAGAGCTTCACTTCTACCGGCGGAGCATGAGGCTCACTTCAGCTTCGAGTGGCTGCC 345
DB 61 AAGAGCTTCACTTCTACCGGCGGAGCATGAGGCTCACTTCAGCTTCGAGTGGCTGCC 120

QY 346 TACCCGGGCTGGTTCCTGTGCAAGCGTGCCTGAAGCCGATCAGCTTGCAGCTCAACCAG 405
DB 121 TACCCGGGCTGGTTCCTGTGCAAGCGTGCCTGAAGCCGATCAGCTTGCAGCTCAACCAG 180

QY 406 CTTCGCCGAGATGGTGGCTGGAATGCCCCATCAAGCTTCTTCCAGCAGTGTGAC 465
DB 181 CTTCGCCGAGATGGTGGCTGGAATGCCCCATCAAGCTTCTTCCAGCAGTGTGAC 240

QY 466 TAG 468
DB 241 TAG 243

RESULT 47
AR221127 985 bp DNA linear PAT 26-SEP-2002
LOCUS AR221127
DEFINITION Sequence 2 from patent US 6426191.

ACCESSION AR221127
VERSION AR221127.1 GI:23328012
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 985)
AUTHORS Ford, J. and Pace, A.
TITLE Assays involving an IL-1 receptor antagonist
JOURNAL Patent: US 6426191-A 2 30-JUL-2002;
FEATURES
source Location/Qualifiers
1..985
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 51.9%; Score 243; DB 6; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.3e-50;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 CCGACTTAACACTAGAGCCAGTGAACATCATGAGCTCTATCTTGGTCCCAAGAAATCC 285
DB 1 CCGACTTAACACTAGAGCCAGTGAACATCATGAGCTCTATCTTGGTCCCAAGAAATCC 60

QY 286 AAGAGCTTCACTTCTACCGGCGGAGCATGAGGCTCACTTCAGCTTCGAGTGGCTGCC 345
DB 61 AAGAGCTTCACTTCTACCGGCGGAGCATGAGGCTCACTTCAGCTTCGAGTGGCTGCC 120

QY 346 TACCCGGGCTGGTTCCTGTGCAAGCGTGCCTGAAGCCGATCAGCTTGCAGCTCAACCAG 405
DB 121 TACCCGGGCTGGTTCCTGTGCAAGCGTGCCTGAAGCCGATCAGCTTGCAGCTCAACCAG 180

QY 406 CTTCGCCGAGATGGTGGCTGGAATGCCCCATCAAGCTTCTTCCAGCAGTGTGAC 465
DB 181 CTTCGCCGAGATGGTGGCTGGAATGCCCCATCAAGCTTCTTCCAGCAGTGTGAC 240

QY 466 TAG 468
DB 241 TAG 243

RESULT 48
AR302955 985 bp DNA linear PAT 12-JUN-2003
LOCUS AR302955
DEFINITION Sequence 2 from patent US 6541623.
ACCESSION AR302955
VERSION AR302955.1 GI:31691555
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 985)
AUTHORS Ford, J., Ho, A.S.Y. and Pace, A.
TITLE Interleukin-1 receptor antagonist and uses thereof
JOURNAL Patent: US 6541623-A 2 01-APR-2003;
FEATURES
source Location/Qualifiers
1..985
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 51.9%; Score 243; DB 6; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.3e-50;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 CCGACTTAACACTAGAGCCAGTGAACATCATGAGCTCTATCTTGGTCCCAAGAAATCC 285
DB 1 CCGACTTAACACTAGAGCCAGTGAACATCATGAGCTCTATCTTGGTCCCAAGAAATCC 60

QY 286 AAGAGCTTCACTTCTACCGGCGGAGCATGAGGCTCACTTCAGCTTCGAGTGGCTGCC 345
DB 61 AAGAGCTTCACTTCTACCGGCGGAGCATGAGGCTCACTTCAGCTTCGAGTGGCTGCC 120

Db 61 AAGAGCTTCACTTCTACCGGCGGAGCATGAGGCTCACTTCCAGCTTGAAGTGGCTGCC 120
QY 346 TACCGGGCTGCTTCTCTGTGCAAGGTGCTGGAAGCCATGAGCTGTGCAACTTCAACCCAG 405
Db 121 TACCGGGCTGCTTCTCTGTGCAAGGTGCTGGAAGCCATGAGCTGTGCAACTTCAACCCAG 180
QY 406 CTTCGCCGAGATGGTGGCTGGAATGCCCCATCAAGACTTCTTCTTCCAGCAGTGTGAC 465
Db 181 CTTCGCCGAGATGGTGGCTGGAATGCCCCATCAAGACTTCTTCTTCCAGCAGTGTGAC 240
QY 466 TAG 468
Db 241 TAG 243
RESULT 49
AX069305 985 bp DNA linear PAT 25-JAN-2001
LOCUS Sequence 2 from Patent WO0102571.
DEFINITION AX069305
ACCESSION AX069305
VERSION AX069305.1 GI:12579177
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1
AUTHORS Ford, J. and Pace, A.
TITLE A interleukin-1 receptor antagonist and uses thereof
JOURNAL Patent: WO 0102571-A 2 11-JAN-2001;
HYSEQ. INC. (US)
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QY 346 TACCGGGCTGCTTCTCTGTGCAAGGTGCTGGAAGCCATGAGCTGTGCAACTTCAACCCAG 405
Db 121 TACCGGGCTGCTTCTCTGTGCAAGGTGCTGGAAGCCATGAGCTGTGCAACTTCAACCCAG 180
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QY 466 TAG 468
Db 241 TAG 243
RESULT 50
BD263574

LOCUS BD263574 295 bp DNA linear PAT 17-JUL-2003
DEFINITION IL-1 related polypeptides.
ACCESSION BD263574
VERSION BD263574.1 GI:33073342
KEYWORDS JP 2002533122-A/8.
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ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1
AUTHORS Goddard, A. and Pan, J.
TITLE IL-1 related polypeptides
JOURNAL Patent: JP 2002533122-A 8 08-OCT-2002;
COMMENT GENE TECH INC
OS Homo sapiens (human)
PN JP 2002533122-A/8
PD 08-OCT-2002
PR 22-DEC-1999 JP 200059118
PR 23-DEC-1998 US 60/113430, 22-JAN-1999 US 60/116843 PR
13-APR-1999 US 60/129122
PI AUBREY GODDARD, JAMES PAN
PC C12N15/09, C07K14/475, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12N15/00, C12N5/00
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FT unsure 283.
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Search completed: January 27, 2006, 21:00:29
Job time : 3030 secs

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RESULT 1	AY413262
LOCUS	AY413262
DEFINITION	AY413262 Homo sapiens ILF5 gene genomic survey sequence
ACCESSION	AY413262.1
VERSION	GI:39769224
KEYWORDS	GSS.
SOURCE	Homo sapiens (human)

ORGANISM	REFERENCE AUTHORS	TITLE	JOURNAL PUBLISHED	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	ORIGIN
Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiinae; Homo.	1 (bases 1 to 468)	Clark, A.G., Gnanowsk, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.J., Adams, M.D. and Cargill, M.	Science 302 (5652), 1960-1963 (2003)	14671302	2 (bases 1 to 468)	Clark, A.G., Gnanowsk, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.J., Adams, M.D. and Cargill, M.	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Matches	468; Conservative 0; Mismatches 0; Indels 0; Gaps 0								
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DEFINITION	TC15434 Human placenta, large insert, pcwv expression library Homo sapiens cDNA clone TC15434 5' similar to Homo sapiens interleukin 1 family, member 5 (delta) (IL1F5), transcript variant 1, mRNA sequence.			
ACCESSION	DR004557	GI:66264430		
VERSION	DR004557			
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.			
AUTHORS	1 (bases 1 to 762)			
TITLE	Bickert,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L., Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M., Zhang,X., Yay,G. and He,W.			
JOURNAL	High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts			
COMMENT	Unpublished (2005)			
	Contact: Kovacs, KF			
	High throughput cDNA Cloning			
	Origene Technologies, Inc. (www.origene.com)			
	6 Taft Court, Suite 100, Rockville, MD 20850, USA			
	Tel: 301 340 3188			
	Fax: 301 340 8606			
	Email: cDNA@origene.com			
	This EST submission is part of an on-going human full-length cloning project at Origene Technologies, Inc.			
	Please contact Origene for access.			
	Origene Technologies, Inc.			
	6 Taft Ct. Suite 100			
	Rockville, MD 20850			
	Tel: (301) 340-3188			
	http://www.origene.com			
	Seq primer: PCMV6 5prime forward vector primer, Origene Technologies Inc.			
FEATURES	Location/Qualifiers			
SOURCE	1..762			
	/organism="Homo sapiens"			
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	/clone="TC15434"			
	/tissue_type="Placenta"			
	/clone_lib="Human placenta, large insert, pcwv expression library"			
	/note="Vector: pCMV6-XL4; Site_1: EcoRI; Site_2: XhoI/SallI compatible end ligatio; Oligo-dt primed reverse transcription optimized for large and GC rich mRNA transcript; cDNA size selection, optimized ligation for large inserts into mammalian expression vector, random clones selected for end sequence verification of full-length genes"			
ORIGIN				
Query Match	100.0%;	Score 468;	DB 8;	Length 762;
Best Local Similarity	100.0%;	Pred. No. 1,7e-118;		
Matches	468;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
1	ATGGTCTCAGAGGGGCGCTGTGCTTCCGATGAAGAACTCGGCATTGAAGGTGCTTTAT	60		
69	ATGGTCTCAGAGGGGCGCTGTGCTTCCGATGAAGAACTCGGCATTGAAGGTGCTTTAT	128		
61	CTGCATTAATTAACAGCTTCTAGACTGGAAGGCTGCATGCAGGGAAGTCAATTAAGTGA	120		
129	CTGCATTAATTAACAGCTTCTAGACTGGAAGGCTGCATGCAGGGAAGTCAATTAAGTGA	188		
121	GAGATCAGCGTGTCTCCCAATGCGTGGCTGATGCCAGCTGTCCCGCTCATCTGGGT	180		
189	GAGATCAGCGTGTCTCCCAATGCGTGGCTGATGCCAGCTGTCCCGCTCATCTGGGT	248		
181	GTCCAGGGGTGAAAGCCAGTGCCTGTCATGTGGGGTGGGCAAGAGCCGACTTAACACTA	240		
249	GTCCAGGGGTGAAAGCCAGTGCCTGTCATGTGGGGTGGGCAAGAGCCGACTTAACACTA	308		

[illegible]

QY 121 GAGATCAGGCTGTCCTCCCATCGTGTGATGTCAGAGCTGTCCTCCCGCTCATCTGGGT 180
 DB 255 GAGATCAGGCTGTCCTCCCATCGTGTGATGTCAGAGCTGTCCTCCCGCTCATCTGGGT 314
 QY 181 GTCCAGGGTGGAGCCAGTGTCTGTCATGTGTGGGGTGGGGCAGAGCCGACTTAACTA 240
 DB 315 GTCCAGGGTGGAGCCAGTGTCTGTCATGTGTGGGGTGGGGCAGAGCCGACTTAACTA 374
 QY 241 GAGCAGGATCATATGAGAGCTCTATCTTGTGTGCAAGGAATCCAGAGCTTCACTTC 300
 DB 375 GAGCAGGATCATATGAGAGCTCTATCTTGTGTGCAAGGAATCCAGAGCTTCACTTC 434
 QY 301 TACCGGCGGAGCATGAGGCTCTCACTTCAGAGCTTCACTTCAGAGCTTCACTTC 360
 DB 435 TACCGGCGGAGCATGAGGCTCTCACTTCAGAGCTTCACTTCAGAGCTTCACTTC 494
 QY 361 CTGTGACGCTGCTGGAAGCCGATCAGCTGTGCACTTCACTTCAGAGCTTCACTTC 420
 DB 495 CTGTGACGCTGCTGGAAGCCGATCAGCTGTGCACTTCACTTCAGAGCTTCACTTC 554
 QY 421 GGCTGGAAATGCCCCCATCAGACTTCTTACTTCCAGAGCTGTGACTAG 468
 DB 555 GGCTGGAAATGCCCCCATCAGACTTCTTACTTCCAGAGCTGTGACTAG 602
 RESULT 4
 LOCUS CR613851 2605 bp mRNA linear HTC 21-JUL-2004
 DEFINITION Full-length cDNA clone CSOD1013YA07 of Placenta Cot 25-normalized
 of Homo sapiens (human).
 ACCESSION CR613851
 VERSION CR613851.1 GI:50494658
 KEYWORDS HTC; cDNA; cDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 2605)
 REFERENCE
 AUTHORS Li, W.B., Gruber, C., Jeesee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 CONTACT : Feng Liang Email : fliang@life.techn.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue
 Redwood City, CA 94063
 2 (bases 1 to 2605)
 REFERENCE
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry-Cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
 COMMENT
 - Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 FEATURES
 Location/Qualifiers
 1..2605
 /organism="Homo sapiens"
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 /clone="CSOD1013YA07"
 /cissue_type="Placenta Cot 25-normalized"
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 Best Local Similarity 100.0%; Pred. No. 2.1e-118;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCTCTGAGTGGGCGCTGTGCTTCCGAATGAAGACTCGGCAATGAAGTGTCTTAT 60
 DB 103 ATGCTCTGAGTGGGCGCTGTGCTTCCGAATGAAGACTCGGCAATGAAGTGTCTTAT 162

QY 61 CTGCATTAATACAGCTTCTAGTGGAGGGCTGCATGACGAGGAGTCTAATAAGTGA 120
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 QY 121 GAGATCAGGCTGTCCTCCCATCGTGTGATGTCAGAGCTGTCCTCCCGCTCATCTGGGT 180
 DB 223 GAGATCAGGCTGTCCTCCCATCGTGTGATGTCAGAGCTGTCCTCCCGCTCATCTGGGT 282
 QY 181 GTCCAGGGTGGAGCCAGTGTCTGTCATGTGTGGGGTGGGGCAGAGCCGACTTAACTA 240
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 DB 343 GAGCAGGATCATATGAGAGCTCTATCTTGTGTGCAAGGAATCCAGAGCTTCACTTC 402
 QY 301 TACCGGCGGAGCATGAGGCTCTCACTTCAGAGCTTCACTTCAGAGCTTCACTTC 360
 DB 403 TACCGGCGGAGCATGAGGCTCTCACTTCAGAGCTTCACTTCAGAGCTTCACTTC 462
 QY 361 CTGTGACGCTGCTGGAAGCCGATCAGCTGTGCACTTCACTTCAGAGCTTCACTTC 420
 DB 463 CTGTGACGCTGCTGGAAGCCGATCAGCTGTGCACTTCACTTCAGAGCTTCACTTC 522
 QY 421 GGCTGGAAATGCCCCCATCAGACTTCTTACTTCCAGAGCTGTGACTAG 468
 DB 523 GGCTGGAAATGCCCCCATCAGACTTCTTACTTCCAGAGCTGTGACTAG 570
 RESULT 5
 LOCUS AL545100 985 bp mRNA linear EST 25-MAR-2004
 DEFINITION AL545100 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens
 clone CSOD1013YA07 5-PRIME, mRNA sequence.
 ACCESSION AL545100
 VERSION AL545100.3 GI:45745585
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 985)
 REFERENCE
 AUTHORS Li, W.B., Gruber, C., Jeesee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On Feb 15, 2001 this sequence version replaced gi:31266936.
 CONTACT : Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
 Email : sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 1383.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?e=CSOD1013YA04QP1&c=1383.f.
 FEATURES
 Location/Qualifiers
 1..985
 /organism="Homo sapiens"
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 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

AUTHORS Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejaritwal, A., Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene titers

JOURNAL Science 302 (5652), 1960-1963 (2003)

REFERENCE 14671302

AUTHORS 2 (bases 1 to 468)

TITLE Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejaritwal, A., Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

source 1..468

gene /organism="Pan troglodytes"

locus /mol_type="genomic DNA"

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ORIGIN

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Best Local Similarity 99.4%; Pred. No. 3.2e-117;

Matches 465; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGTCCTGAGTGGGGCGCTGCTGCTCCGAATGAAGAGCTCGGACATTAAGTCTTAT 60

DB 1 ATGGTCCTGAGTGGGGCGCTGCTGCTCCGAATGAAGAGCTCGGACATTAAGTCTTAT 60

QY 61 CTGCATTAATTAACAGCTTCTAGCTGAGAGGCTGCATGACGAGAGGCTTTAAAGTGTA 120

DB 61 CTGCATTAATTAACAGCTTCTAGCTGAGAGGCTGCATGACGAGAGGCTTTAAAGTGTA 120

QY 121 GAGATCAGGCTGCTCCCAATCGTGGTGGATGCCAGCTGTCCCGCTCATCTCGGT 180

DB 121 GAGATCAGGCTGCTCCCAATCGTGGTGGATGCCAGCTGTCCCGCTCATCTCGGT 180

QY 121 GAGATCAGGCTGCTCCCAATCGTGGTGGATGCCAGCTGTCCCGCTCATCTCGGT 180

DB 121 GAGATCAGGCTGCTCCCAATCGTGGTGGATGCCAGCTGTCCCGCTCATCTCGGT 180

QY 181 GTCCAGGGGTGAAGCAGTGGCTGCTGATGTGGGGCGGGCAGAGCCGACTTAACACTTA 240

DB 181 GTCCAGGGGTGAAGCAGTGGCTGCTGATGTGGGGCGGGCAGAGCCGACTTAACACTTA 240

QY 241 GAGCAGTGAACATCATGAGCTCTATCTTGGTGCACAGAGATCCAGAGCTTCACTTC 300

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QY 241 GAGCAGTGAACATCATGAGCTCTATCTTGGTGCACAGAGATCCAGAGCTTCACTTC 300

DB 241 GAGCAGTGAACATCATGAGCTCTATCTTGGTGCACAGAGATCCAGAGCTTCACTTC 300

QY 301 TACCGGCGGAGCATGGGCTCACTTCAGCTTCAGAGTGGCTTACCCGGGCTGGTTC 360

DB 301 TACCGGCGGAGCATGGGCTCACTTCAGCTTCAGAGTGGCTTACCCGGGCTGGTTC 360

QY 301 TACCGGCGGAGCATGGGCTCACTTCAGCTTCAGAGTGGCTTACCCGGGCTGGTTC 360

DB 301 TACCGGCGGAGCATGGGCTCACTTCAGCTTCAGAGTGGCTTACCCGGGCTGGTTC 360

QY 361 CTGTGACAGGTGCTGAGAGCCGATCAGCTGTGCAACTACACCAAGTTCAGAGATGT 420

DB 361 CTGTGACAGGTGCTGAGAGCCGATCAGCTGTGCAACTACACCAAGTTCAGAGATGT 420

QY 421 GCGTGAATGCCCCCATCAGACTTCTTACTTCCAGCAGTGTGACTAG 468

DB 421 GCGTGAATGCCCCCATCAGACTTCTTACTTCCAGCAGTGTGACTAG 468

RESULT 8

LOCUS BIO89828 726 bp mRNA linear EST 20-JUN-2001

DEFINITION 602855071p1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4996432 5'

ACCESSION BIO89828

VERSION BIO89828.1 GI:14508158

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLM11021 row: n column: 17
High quality sequence stop: 709.

FEATURES

source 1..726

gene /organism="Homo sapiens"

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/cell_line="MGC36"

/lab_host="DH10B"

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/note="Organ: cervix; Vector: pCMV-Sport6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 Kb. Library prepared by Life Technologies."

ORIGIN

Query Match 97.9%; Score 458; DB 2; Length 726;

Best Local Similarity 100.0%; Pred. No. 9.7e-116;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GTGGGGCGCTGTGCTTCCGAATGAAGAGCTCGGACATTAAGTCTTATCTGCATTA 70

DB 1 GTGGGGCGCTGTGCTTCCGAATGAAGAGCTCGGACATTAAGTCTTATCTGCATTA 70

QY 71 ACCAGCTTACTGAGAGGGCTGCATGACGAGGAGGCTCTTAAGGTGAAGATCAGCG 130

DB 71 ACCAGCTTACTGAGAGGGCTGCATGACGAGGAGGCTCTTAAGGTGAAGATCAGCG 130

QY 61 ACCAGCTTACTGAGAGGGCTGCATGACGAGGAGGCTCTTAAGGTGAAGATCAGCG 120

DB 61 ACCAGCTTACTGAGAGGGCTGCATGACGAGGAGGCTCTTAAGGTGAAGATCAGCG 120

QY 131 TGGTCCCAATGAGTGGTGGTGCATGACGAGCTGTCCCGCTCATCTGGGTGTCAAGGTG 190

DB 131 TGGTCCCAATGAGTGGTGGTGCATGACGAGCTGTCCCGCTCATCTGGGTGTCAAGGTG 190

QY 121 TGGTCCCAATGAGTGGTGGTGCATGACGAGCTGTCCCGCTCATCTGGGTGTCAAGGTG 180

DB 121 TGGTCCCAATGAGTGGTGGTGCATGACGAGCTGTCCCGCTCATCTGGGTGTCAAGGTG 180

QY 191 GAAGCAGTGTCTGATGTGGGGTGGGCGAGAGCCGACTTAACACTAGAGCCAGTGA 250

DB 191 GAAGCAGTGTCTGATGTGGGGTGGGCGAGAGCCGACTTAACACTAGAGCCAGTGA 250

QY 181 GAAGCAGTGTCTGATGTGGGGTGGGCGAGAGCCGACTTAACACTAGAGCCAGTGA 240

DB 181 GAAGCAGTGTCTGATGTGGGGTGGGCGAGAGCCGACTTAACACTAGAGCCAGTGA 240

QY 251 ACATGAGAGCTCATCTGTGTGCAAGAGATCCAGAGCTTCACTTACCGGCGGG 310

DB 251 ACATGAGAGCTCATCTGTGTGCAAGAGATCCAGAGCTTCACTTACCGGCGGG 310

QY 241 ACATGAGAGCTCATCTGTGTGCAAGAGATCCAGAGCTTCACTTACCGGCGGG 300

DB 241 ACATGAGAGCTCATCTGTGTGCAAGAGATCCAGAGCTTCACTTACCGGCGGG 300

QY 311 ACATGGGGCTCACTTCAGCTTCAGAGTGGCTTACCCGGGCTGGTTCCTGTGACCG 370

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QY 301 ACATGGGGCTCACTTCAGCTTCAGAGTGGCTTACCCGGGCTGGTTCCTGTGACCG 360

DB 301 ACATGGGGCTCACTTCAGCTTCAGAGTGGCTTACCCGGGCTGGTTCCTGTGACCG 360

QY 371 TGGCTGAAGCCGATCAGCTGTGCAACTACCAAGCTTCCGAGATGTGGCTGAATG 430

DB 371 TGGCTGAAGCCGATCAGCTGTGCAACTACCAAGCTTCCGAGATGTGGCTGAATG 430

QY 361 TGGCTGAAGCCGATCAGCTGTGCAACTACCAAGCTTCCGAGATGTGGCTGAATG 420

DB 361 TGGCTGAAGCCGATCAGCTGTGCAACTACCAAGCTTCCGAGATGTGGCTGAATG 420

QY 431 CCCCATCAGAGACTTCTACTTCCAGCAGTGTGACTAG 468

DB 431 CCCCATCAGAGACTTCTACTTCCAGCAGTGTGACTAG 468

QY 421 CCCCATCAGAGACTTCTACTTCCAGCAGTGTGACTAG 458

DB 421 CCCCATCAGAGACTTCTACTTCCAGCAGTGTGACTAG 458

RESULT 9

LOCUS	1199 bp	mRNA	linear	HTC 03-APR-2000
DEFINITION	AK008977			
ACCESSION	AK008977			
VERSION	AK008977.1	GI:12843490		
KEYWORDS	HTC, CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1			
TITLE	Carninci, P. and Hayashizaki, Y.			
JOURNAL	High-efficiency full-length cDNA cloning			
PUBMED	Mech. Enzymol. 303, 19-44 (1999)			
REFERENCE	10349636			
AUTHORS	2			
TITLE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
PUBMED	Genome Res. 10 (10), 1617-1630 (2000)			
REFERENCE	11042159			
AUTHORS	3			
TITLE	Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kikuna, T., Tashiro, H., Itoh, M., Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, R., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Marahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.			
JOURNAL	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer			
PUBMED	Genome Res. 10 (11), 1757-1771 (2000)			
REFERENCE	11076661			
AUTHORS	4			
TITLE	The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.			
JOURNAL	Functional annotation of a full-length mouse cDNA collection			
PUBMED	Nature 409, 685-690 (2001)			
REFERENCE	5			
AUTHORS	The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.			
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs			
JOURNAL	Nature 420, 563-573 (2002)			
PUBMED	6 (bases 1 to 1199)			
REFERENCE	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoaka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kaubawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takehashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Yamamatsu, M. and Hayashizaki, Y.			
JOURNAL	Direct Submission			
PUBMED	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)			
COMMENT	Please visit our web site (http://genome.gsc.riken.jp/) for further details.			
	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.			

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'] GAGAGAAGAAATCCCAAGGCTCTTTTCTTTTTTCTTN 3'), cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'] GAGGAGAAGATTCTCGAGTTAATTAATTAATCCCCCCCCC 3'). cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.

Host: SOLR.

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                        /db_xref="taxon:10090"
                        /clone="2210418104"
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ORIGIN
Query Match       75.0%; Score 351.2; DB 4; Length 1199;
Best Local Similarity 84.4%; Pred. No. 4,3e-86;
Matches 395; Conservative 0; Mismatches 73; Indels 0; Gaps 0

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        193 CTGCACAATAACCAAGCTCTGAGCTGGAAGACTGCACG CAGAGAGTCAATTAAAGTGA 252
      121 GAGATCACAGTGTGCTCCCAATCGAGGCTGAGATGTCAG CACTGTGCCCTCATCTCGGAT 180
        253 GAGATCAAGTGTGTCCCAAATCGGCACTGGAATGCCA GTCTGTGCCCTGTCAATCTTGAGC 312
      181 GTCCAGGCTGAAGCCAGTGCCTGTCAATGTGGGAGTGG GCGGACAGAACCCACTTAAACATA 240
        313 GTTCAAGGAGGAAGCCAAGTGCCTATCTGTGGGACA GAGAAAGGCCCAATTCTGAACATT 372
      241 GAGCCAGTGAACATCATGATGAGCTGTATTTGGTGC CAAGAAATCAAGAAGCTTACCCTTC 300
        373 GAGCCAGTGAACATCATGATGAGCTGTATCTCGAGGCG CAAAGGAATCAAGAAGCTTACCCTTC 432
      301 TACGGGGGGGACATGGGGGCTCACTCCGACGTTCCAG TGAGTGCGCTCAACCGGGGCTGGTTC 360
        433 TACGGGGGGGACATGGGGGCTCTTAACCTCCACGCTTC CAGATCCGCTCTACCAAGGCTGGTTC 492
      493 CTGTGCAAGTGTGCTGTAAGCCGATCAGGCTGTCAAG ACTCACCACCAAGTATGAT 420
        553 GCCTGGAGTGTCCCATCACAGACTTCACTTTCAGCAGT GTGACTAG 600
    
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DEFINITION  AGENCOURT_12780806 NIH_MGC_136 Mus musculus cDNA clone
IMAGE:30286859 5', mRNA sequence.
ACCESSION   CB590160
VERSION     CB590160.1 GI:29508016
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 862)
AUTHORS    NIH-MGC http://mgi.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Dr. David Rowe
            cDNA Library Preparation: Invitrogen Corp
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM321 row: m column: 12
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            Location/Qualifiers
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                /clone_lib="NIH_MGC_136"
                /note="Vector: pCMV-SPORT6.1; Site.1: EcoRV; Site.2: NotI;
                Normalized, full-length enriched library from pool of
                mouse embryonic limb, maxilla and mandible, embryonic day
                17.5, 18.5 and newborn (mandible (5, 4 and 1 limb and jaw
                equivalents from respective days). Cloned directionally,
                oligo-dT primed (5'-GACTAGTCTGATGCGGCGGCC(17)15-3'.
                Size selected for the >1kb fragments, average insert size
                1.2 kb. Normalization to Cot 7.5. Tissue contributed by
                David Rowe; library constructed by Resgen, Invitrogen
                Corp. Note: this is a NIH_MGC library."

FEATURES
    source

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Query Match      74.7%; Score 349.6; DB 6; Length 862;
Best Local Similarity 84.2%; Pred. No. 1.1e-85;
Matches 394; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

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61  CTGCATTAATTAACCACTTCTAGCTGAGAGGCTGCATGACGAGGAGTCAATTAAGTGA 120
145  CTGCACATTAACCACTGCTGCTGAGGAGACTGCACGACGAGAAGTCAATTAAGTGA 204

121  GAGATCAGCGTGTCTCCCAATCGGTGGCTGATGCCAGCTGTCCCGCTCATCTGGGT 180
205  GAGATCAGTGTGTCCCAATCGGGGCACTGATGCCAGTCTGTCCCTGTCACTCGGGC 264
181  GTTCAGGGTGAAGCCAGTGTCTGTCATGTGGGTGGGCGGACAGGCCGACTTAACAC 240
265  GTTCAAGGAGGAGCCAGTGTCTTGTGGACAGAGAAAGGGCAATTTGAAACTT 324
241  GAGCCAGTAACATCATGAGCTCTATCTTGGTCCAGAGAAATCCAAAGCTTCACTTC 300
325  GAGCCAGTAACATCATGAGCTCTAATCTCGGGGCGCAAGAAATCAAAAGCTTCACTTC 384
301  TACCGCGGGAGACATGGGGCTCACTTCAGCTTGAAGTGGCTGAGTCCCGGGCTGGTTC 360
385  TACCGCGGGAGATATGGGTCTTAATCTCAAGCTTGAATCGGTGCTTCAACCAAGCTG 444

DEFINITION  AGENCOURT_12770733 NIH_MGC_136 Mus musculus cDNA clone
IMAGE:30286810 5', mRNA sequence.
ACCESSION   CB589411
VERSION     CB589411.1 GI:29507267
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 885)
AUTHORS    NIH-MGC http://mgi.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Dr. David Rowe
            cDNA Library Preparation: Invitrogen Corp
            DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM321 row: k column: 11
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                /note="Vector: pCMV-SPORT6.1; Site.1: EcoRV; Site.2: NotI;
                Normalized, full-length enriched library from pool of
                mouse embryonic limb, maxilla and mandible, embryonic day
                17.5, 18.5 and newborn (mandible (5, 4 and 1 limb and jaw
                equivalents from respective days). Cloned directionally,
                oligo-dT primed (5'-GACTAGTCTGATGCGGCGGCC(17)15-3'.
                Size selected for the >1kb fragments, average insert size
                1.2 kb. Normalization to Cot 7.5. Tissue contributed by
                David Rowe; library constructed by Resgen, Invitrogen
                Corp. Note: this is a NIH_MGC library."

FEATURES
    source

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Db		205	GAGATCATGTTGTTCCTCCAAATCGGGCACA GAGATTACCA GTCTGTGCCCTTGTCATCTCTGGCC	264
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Db		325	GAGCCAGTGAACATCATGTAGAGCTCTTACTCTGGGGCTCAAAGAAATCAAAAGCTTCAACCTTC	384
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Db		385	TACCGGGCGGGA TATGGGTCTTAACCTCCAGCTTCGAAATCGGTGGCTACCAAGGGCTGGTTC	444
Oy		361	CTGTGCACAGTGGTCTCTGAAGCCGATAGCTGT CAGACTCACCCAGCTTCCCAGAGATGCT	420
Db		445	CTGTGCACCTCAACC CGAAGCTGACCAAGCCTGTCAAGGCTC ACTCTAGATCCCTGAGAGAACCC	504
Oy		421	GGCTGGAAATGCCCCCATCAAGACTTCACTTCCAGCAGTGTGACTAG	468
Db		505	GCTGGAGTGTCTCCATCAAGACTTCACTTCAAGCAGTGTGACTAG	552
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DEFINITION				
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AUTHORS
 Adachi,T., Aizawa,K., Akahira,S., Akimura,T., Arii,A., Aono,H.,
 Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
 Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hizomoto,K.,
 Hirooka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
 Kikuchi,T., Kato,H., Kawai,J., Kojima,Y., Komuro,H., Kouida,M.,
 Koye,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Niimi,K.,
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 Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Saeki,D.,
 Shibata,K., Shibata,Y., Shingawa,A., Shitaki,T., Sogabe,Y.,
 Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
 Tejima,Y., Toyota,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
 Yoshino,M., Yumatsugu,M. and Hayashizaki,Y.
TITLE
 Direct Submission
JOURNAL
 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
 url: http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
 Fax:81-45-503-9216)
COMMENT
 On Dec 6, 2002 this sequence version replaced gi:12852516.
 Please visit our web site (http://genome.gsc.riken.jp/) for further
 details.
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues. First strand cDNA was primed with a primer
 [5' GAGAGAGAGAAGATCCAAAGAGCTCTCTTTTCTTTTCTTTTNN 3'], cDNA was
 prepared by using trihalose thermo-activated reverse transcriptase
 and subsequently enriched for full-length by cap-trapper. cDNA went
 through one round of normalization to Rot = 10.0 and subcloning to
 Rot = 100.0. Second strand cDNA was prepared with the primer
 adapter of sequence [5'
 GAGAGAGATCTTCGAGTTAATTAATTAATATCCCCCCCCCC 3']. cDNA was cleaved
 with BamHI and XhoI. cDNA of size complemented longer than 7 kb was
 selected before cloning. Vector: a modified plasmid pBluescript KS(+) after
 bulk excision from Lambda FLC 1. Cloning sites, 5' end: SalI, 3'
 end: BamHI. Host: DH10B.
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 Best Local Similarity 84.4%; Pred. No. 3,9e-83;
 Matches 395; Conservative 0; Mismatches 72; Indels 1; Gaps 1;
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DEFINITION	BY709379 RIKEN full-length enriched, adult male tongue Mus musculus cDNA clone Z310041K07 5', mRNA sequence.			
ACCESSION	BY709379			
VERSION	BY709379.1	GI:27120580		
KEYWORDS	EST.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.			
AUTHORS	Okazaki, Y., Furuno, N., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Otsuo, N., Saito, R., Suzuki, H., Yamana, I., Kiyouasa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bulc, C., Hune, D.A., Quackenbush, J., Schmitt, L.M., Kanapin, A., Matuda, H., Batelov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brasic, V., Chochiaia, C., Corbani, L.E., Cousins, S., Dalla, E., Deganti, T.A., Pletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godik, A., Gough, J., Grimond, S., Guestindich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasaki, Y., Kedzietski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lemhard, B., Lyons, P.A., Meglath, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavani, W.J., Perce, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, U.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shinada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanebe, Y., Wells, C., Wilting, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashihime, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shimagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.			
JOURNAL	Nature	420,	563-573	(2002)
PUBMED	12466851			
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suihiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-fesgsc.riken.jp, URL:http://genome.gsc.riken.jp/			

FEATURES

source

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/note=Title 1: XhoI; Site 2: SclI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5']
GAGGAGGAGAAGATCCAAAGCTCTTTTTCCTTTTTTN 3'. cDNA was prepared by using tris(phenyl)thio-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5']
GAGGAGGAGATTTCGGATTATTAATTAATTCCTCCCCCCCCC 3'. cDNA was cleaved with XhoI and SclI."

ORIGIN

Query Match 72.3%; Score 338.4; DB 5; Length 708;
Best Local Similarity 82.7%; Pred. No. 1.4e-82;
Matches 387; Conservative 0; Mismatches 81; Indels 0; Gaps 0

Db

1 ATGTCTCGTAGTGSGGCGCTGCTTCGCCAATGAAGACATCGGCATTGAAGTGCCTTAT 60
233 ATGGTTCTGAGTGSGGCACTATGCTCCGAATGAAGATTCAGCTTGAAAGTACTGTAAT 292
61 CTGCATAATTAACCACTTCTAGCTGAGAGGCGTCGATGACGGGAAGGTCAATTAAGGTGA 120
233 CTGCACAATTAACCACTGCTGAGCTGAGAGCATGCAACGACGAAGAAGGTCAATTAAGGTGAG 352
121 GAGATCAGCGTGTGCTCCCAATCGGTGAGTGCAGCTGTCCCGCTCATCTCTGAGGT 180
Db 353 GAGATCAGTGTGTGCTCCCAATCGGACATGCAATGCCAGTCTGTCCCCTTCATCTCGGGC 412
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FEATURES	Source
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Db	553 CTGTGACCTTACCGGAGAGCTGACAGGCTGTGACGCTTCACTCAAGAACCTTGAGGACCC
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LOCUS	CR742272
DEFINITION	CR742272 Soares parathyroid tumor NbHRA Homo sapiens cDNA clone
ACCESSION	U00000.1
VERSION	CR742272.1
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 414)
AUTHORS	Ebert, L., Hell, O., Hennig, S., Korn, B., Neubert, P., Partsch, E., Peters, M., Radeflo, U. and Schneider, D.
TITLE	I. M. A. G. E. cDNA Clone Collection
JOURNAL	Unpublished (2004)
COMMENT	Contact: Inge Ariart RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Email: www.rzpd.de RZPD: IMAGP998M234181. RZPDLIB: I. M. A. G. E. cDNA Clone Collection; Contact: Inge Ariart RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel: +49 30 32639 100 Fax: +49 30 32639 111 www.rzpd.de This clone is available royalty-free from RZPD. contact RZPD (clone: rzd04) for further information. Seq primer: M13u, Primer sequence: GTGTGTAACGACGCGCAGT. Location/Qualifiers 1..414 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGP998M234181 ; IMAGE:1647934" /tissue_type="parathyroid tumor" /dev_stage="adult" /lab_host="DH10B (ampicillin resistant)" /clone_1ib="Soares parathyroid tumor NbHRA" /note="Organ: parathyroid gland; Vector: pT7T3D (pharmacia) with a modified polylinker; Site1: Not I; Site2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer 15'-TGTACCAATCTGAAATGAGGCGCGACCAATTTTTTTTTTTTTTTTTTTT TTTTT-3', double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3D vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,

ORIGIN	NIH."
Query Match	72.2%; Score 338; DB 7; Length 414;
Best Local Similarity	99.1%; Pred. No. 1.6e-82;
Matches 349; Conservative	0; Mismatches 2; Indels 1; Gaps 1;
Dy	1 ATGTGCTCGATGGGGGCGCTGTGCTTCCGATGAAGACCTCGGCTTAAGTGTCTTTAT 60
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Dy	121 GAGATCAGCGTGTGCCCAATCGGTGGCTGGATCCAGCGCTGTCCCGTCATCTGGGT 180
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	RESULT 16
LOCUS	AK010020
DEFINITION	AK010020 1531 bp mRNA linear HTC 03-APR-2004
ACCESSION	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310063B08 product:interleukin 1 family, member 5 (delta), full insert sequence.
VERSION	AK010020
KEYWORDS	AK010020.1 GI:12845175
SOURCE	HTC; CAP trapper. Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 10349636
AUTHORS	2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 11042159
JOURNAL PUBMED	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Niishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujisake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, D., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system -384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 11076661
JOURNAL PUBMED	4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
REFERENCE	
AUTHORS	

Db 1 AATGAGATTCAGCTTGAGGTAAGTACTGATCTGACAAATAACACAGCTGCTGGAGG 60
 QY 90 GGTGATGAGGAGGAGTATTAAGTAAAGATCACCGTGTCTCCCAATCGTGCT 149
 Db 61 ACTGACGAGAGAGAGTATTAAGTAAAGATGAGATGATGTTGTCCCAATCGGAGCT 120
 QY 150 GGATGCGAGCTGTCTCCCGTCACTCTGGGGTGTCAAGGTGAGAGCAATGCTGTCTG 209
 Db 121 GGATGCGAGCTGTCTCCCGTCACTCTGGGGTGTCAAGAGAGCAATGCTGTCTG 180
 QY 210 TGGGGTGGGCGAGAGCCGACTCTTAACACTAGACCAATGATCATGAGCTTATCT 269
 Db 181 TGGGACAGAGAGAGAGGCGCAATCTGAACTTGAGCCAGTGAACATCATGAGCTTACCT 240
 QY 270 TGGTGCAGAGAAATCCAAAGAGCTTCACTTCAACCGGCGGAGCATGGGGCTCACTCCG 329
 Db 241 CCGGGCGCAAGAGAAATCAAGAGCTTCACTTCAACCGGCGGAGATGAGCTTCACTCCG 300
 QY 330 CTTCGAGTGGGCTGCTTACCCGCGCTGTCTCTGTCAGAGTGCCTGAAGCCGATCAGCC 389
 Db 301 CTTCGAGTGGGCTGCTTACCCGCGCTGTCTCTGTCAGAGTGCCTGAAGCCGATCAGCC 360
 QY 390 TGTCAAGCTCACCCAGCTTCCGAGAGATGAGTGGTGAATGCCCGCATGACAGATTCTTA 449
 Db 361 TGTCAAGCTCACCTCAAGATCCCTGAGAGACCCCGCTGGATGCTCCCATCAGACATTCTTA 420
 QY 450 CTTCAGGAGCTGTGACTAG 468
 Db 421 CTTCAGGAGCTGTGACTAG 439

RESULT 18
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 DEFINITION DKFZp686022193_r1 686 (synonym: h1cc3) Homo sapiens cDNA clone
 BX477358
 ACCESSION DKFZp686022193 5', mRNA sequence.
 VERSION BX477358
 KEYWORDS BX477358.1 GI:31674556
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 REFERENCE 1 (bases 1 to 338)
 AUTHORS Anseuge,W., Krieger,S., Regiert,T., Rittmüller,C., Schwager,B.,
 Mewes,H.W., Weill,B., Amid,C., Osanger,A., Fobbo,G., Han,M. and
 Wiemann,S.
 TITLE EST (Anseuge,W., Krieger,S., Regiert,T., Rittmüller,C., et al.)
 JOURNAL Unpublished (2003)
 COMMENT Contact: MIPS
 MISC
 Ingelstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;
 sequenced by EMBL (European Molecular Biology Laboratories,
 Heidelberg/Germany) within the cDNA sequencing consortium of the
 German Genome Project.
 No 31 sequence available.
 This clone (DKFZp686022193) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
 Location/Qualifiers

FEATURES

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 /db_xref="taxon:9606"
 /clone="DKFZp686022193"
 /dev_stage="adult"
 /lab_host="DH10B"
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 /note="Vector: pTribex2; site_1: sf1a; site_2: sf1b;
 Location/Qualifiers

ORIGIN

cDNA-collection"

Query Match 57.9%; Score 271; DB 5; Length 338;
 Best Local Similarity 100.0%; Pred. No. 5,6e-64;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTAGTGGGGCGCTGTGCTTCGAAATGAAGACTCGGCAATTGAAGGCTTTAT 60
 Db 68 ATGGCTCTAGTGGGGCGCTGTGCTTCGAAATGAAGACTCGGCAATTGAAGGCTTTAT 127
 QY 61 CTGCATATATACAGCTTTCTAGCTGAGGGCTGTCATGAGGAGTCAATTAAGGTGA 120
 Db 128 CTGCATATATACAGCTTTCTAGCTGAGGGCTGTCATGAGGAGTCAATTAAGGTGA 187
 QY 121 GAGATCAGCTGTGCTCCCAATGCTGTGATATGCCAGCTGTCCCGCTCATCTGGGT 180
 Db 188 GAGATCAGCTGTGCTCCCAATGCTGTGATATGCCAGCTGTCCCGCTCATCTGGGT 247
 QY 181 GTCCAGGGTGAAGACGAGTCCGTGATGTGGGGTGGGCGAGGCGGACTTAACACTA 240
 Db 248 GTCCAGGGTGAAGACGAGTCCGTGATGTGGGGTGGGCGAGGCGGACTTAACACTA 307
 QY 241 GAGCCAGTGAACATCATGAGGCTTATCTTG 271
 Db 308 GAGCCAGTGAACATCATGAGGCTTATCTTG 338

RESULT 19
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 DEFINITION AGENCOURT_11259798 NIH MGC_135 Mus musculus cDNA clone
 IMAG:30135655 5', mRNA sequence.
 ACCESSION CB194288
 VERSION CB194288
 KEYWORDS CB194288.1 GI:28218671
 EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 898)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
 TITLE NIH-MGC
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: Dr. David Rowe
 cDNA Library Preparation: Invitrogen Corp
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: NDAM0034 row: a column: 08
 High quality sequence start: 16
 High quality sequence stop: 652.
 Location/Qualifiers

FEATURES

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 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH MGC 135"
 /note="Vector: pCMVSPORT6.1; Site 1: EcoRV; Site 2: NotI;
 Normalized full-length enriched library from pooled mouse
 embryonic limb, maxilla and mandible, day 12.5, 13.5,
 14.5, and 15.5 (size selected for the 0.5-1 kb fragments)
 Cloned directionally, priming method: Oligo-dT. cDNA
 enrichment: >1k bp, Average insert size 1.6k bp.
 Normalization (Cot value): 7.5 kb. Priming sequence:
 5' GACTAGTTTCAATCGCAGCGCCGCCCT(T) 3' Tissue contributed

Oy	128	GCSTGGTCCCAATCGGTGGCTGGAAATGCGACGCTGGCCCCCGATCTCGGGGTGCAG	187
Db	1	GTGTTGTCCCAATGGGGCACTGGATGCCAGTGTGTCCCTTGATCTCGGGGCTTCAG	60
Oy	188	GTGAAAGCCAGTGCCTGTCTATGTGGGGTGGGGGAGAGGCCGACTCTTAACCTAGACCAG	247
Db	61	GAGGAAGCGAGTGCCCTATCTTGTGGGACAGAGAAAGGCGCAATTGAAACTTGAACCG	120
Oy	248	TGAACATCATGAGCTCTATCTTTGGTGGCCAAGGAATCCAAGACTTCACCTTCTACCGG	307
Db	121	TGAACATCATGAGCTCTACTCTGGGGGCAAGGAATCAAGAAGCTTCACCTTCTACCGG	180
Oy	308	GGGACATGGGGCTCACCTTCAGACTTCGAAGTCGGCTGCTCAACCGGGCTGGTTCCTGTCA	367
Db	181	GGGAATATGGGTCTTACCTTCACACTTCGAATTCGGCTGCCTTACCCAGGGCTGGTTCCTGTCA	240
Oy	368	CGGTGCTTGAAGCCGATCGAGCTGTCAGACTCAACCCAGCTTCCCGAAGATGGGTGGTGA	427
Db	241	CCTCACCGGAAGCTGACCGCTGTGTAAGGCTCACTCAGATCCCTTGAAGACCCCGCTGGG	300
Oy	428	ATGCCCCATCAGAGCTTCTACTTCCACAGTGTGACTAG	468
Db	301	ATGCTCCCATCAGAGCTTCTTACTTTCACAGACTGTGACTAG	341

RESULT 21	LOCUS	DEFINITION	606 bp	mRNA	linear	EST 16-DEC-2007
BY708859	BY708859	musculus full-length cDNA clone 2210418104 5', mRNA sequence.				
ACCESSION	BY708859					
VERSION	BY708859.1	GI:27120053				

SOURCE ORGANISM	Mus musculus (house mouse)
	Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE AUTHORS

TITLE Analysis of the mouse transcriptome based on functional annotation

JOURNAL
PUBMED

COMMENT
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: gene-rescsc.riken.jp, URL: <http://genome.gsc.riken.jp/>
Adachi J., Aizawa K., Akimura, T., Arkawa, T., Carninci, P.,
Fukuda S., Hashizume W., Hayashida K., Hirosewa, T., Hori, F.,
Imomani K., Ishii Y., Itoh M., Kageura K., Kawai, J., Kojima, Y.,
Kondo, S., Konno H., Koya S., Miyazaki, A., Murata, M., Nakamura, M.,
Nomura K., Numazaki, R., Ono, M., Oshiro, N., Saito, T., Sakazume, N.,
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Teganu, W.,
Takeuchi, Y., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y.

Computational Analysis of Full-length Human cDNAs Compared with Human Genome Sequences. *Mamm. Genome*. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)

RIKEN integrated sequence (RISA) system—384-format sequencing pipeline with 384 multichannel sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and genome science laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

```

/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="2210418104"
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/tissue_type="stomach"
/dev_stage="adult"
/lab_host="SOLR"
/clone_11b="RIKEN full-length enriched, adult male
stomach"
/note="Site_1: XhoI; Site_2: SstI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGGAGAGGCGCGCGACACTGAGCTTTTTTTTTTTNN 3'], cDNA was
prepared by using trihalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGAGGAGACATTCGACGTAATTAATTAATATCCCCCCCCCCC 3']. cDNA
was cleaved with XhoI and SstI."

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ORIGIN

Query Match	51.0%;	Score 238.8;	DB 5;	Length 686;
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Best Local Similarity  82.1%;  Fied. NO. 3.4e-55;
Matches 299;  Conservative  0;  Mismatches  62;  Indels  3;  Gaps  2

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1 ATGTCCTGAGTGGGCGCTGTCTCCGATGAAGGACTGGCATTGAAGGTCCTTTAT 60

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193 CTGCACATTAACGAGCTGCTGGCTGGAGGACTGCACCGCAGAGGTCACTTAAGGTGAG 252

121 GAGATCAGCGTGTTCCCCAATCGGTGCTGATGCCAGCCTGTCCCCCGTATCTGGGT 180

Db 253 GAGATCATGTTGTCTCCAAATGGGCACTGATGCGAGTCTGTCCCTGTACTCTGGGC 312

Qy 181 GTCCAGGGTGAAGCCAGTGGCTCTCATGTGGGGGCGAGAGCCGACTTAACTA 240

Db 313 GTTCAAGAGAGAGAGGAGGAGGCTTATCTTGTGGACAGAGAAAGGCGCAATCTGAACTT 372

Qy 241 GAGCCAGTGAACATCATGAGAGCTTATCTGTGGTGCAGAGAAATCCAGAGCTTCACTTC 300

Db 373 GAGCCAGTGAACATCATGAGAGCTTATCTGTGGGCGCCAGAAATCAAAGAGCTTCACTTC 432

Qy 301 TACCGCGGAGCATGAGGCG-TCACCTCCAGCTT--CGAGTCGGCTGCTTACCCGGGCTGG 357

Db 433 TTCGGCGGAGATGGGCTTTTACCTCCAGCTTTGGAAATCCGGTTGCTATCCCAAGGCTGG 492

Qy 358 TTCC 361

Db 493 TTTT 496

RESULT 22 382 bp mRNA linear EST 05-SEP-1996

LOCUS W08205 mb49b1.r1 Soares mouse p3JNMFR19.5 Mus musculus cDNA clone

DEFINITION IMAGE:332733 5' similar to PIR:A49031 A49031 interleukin 1 receptor antagonist - mouse ; mRNA sequence.

ACCESSION W08205

VERSION W08205.1 GI:1282415

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 382)

AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gettel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE The WashU-HHMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:214133
Seq primer: EST primer
High quality sequence stop: 354.

FEATURES

source

1..382

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/note="Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-GGTACCATCTGAGTGGAGCGGCGGCGCATTTTCTTTTCTTTT 3'] , double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a C_{ot} = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by

ORIGIN Dr. Minoru Ko (Wayne State University)."

Query Match 44.6%; Score 208.6; DB 8; Length 382;

Best Local Similarity 84.2%; Pred. No. 1,1e-46;

Matches 235; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 1 ATGGCTCGAGTGGGGCGCTGTGCTTCCGAATGAAGAGCTGGCATTAAGTGTAT 60

Db 104 ATGGCTCGAGTGGGGCGCTGTGCTTCCGAATGAAGAGTTCAGCTTGAAGTAT 163

Qy 61 CTGCATTAATTAACACAGCTTCTAGCTGAGGGCTGCATGCAAGAGCTATTAAAGTGA 120

Db 164 CTGCACATTAACAGAGCTCTGCTGAGAGAGCTGCACGACAGAAAGGTATTAAAGTGA 223

Qy 121 GAGATCAGCTGTGCTCCCAATCGGTGGCTGATGTCACCTGTCCCGGTACTCTGGGT 180

Db 224 GAGATCAGCTGTGCTCCCAATCGGTGGCTGATGTCACCTGTCCCGGTACTCTGGGT 283

Qy 181 GTCCAGGGTGAAGCCAGTGCCTGTCTATGTGGGGGCGAGAGCCGACTTAACTA 240

Db 284 GTTCAAGAGAGAGAGCCAGTGCCTTATCTTGTGGGACAGAGAAAGGCGCAATCTGAACTT 343

Qy 241 GAGCCAGTGAACATCATGAGAGCTTATCTTGGTGGCAAG 279

Db 344 GAGCCAGTGAACATCATGAGAGCTTATCTTGGTGGCAAG 382

RESULT 23 348 bp mRNA linear EST 07-DEC-2002

LOCUS BY109350 RIKEN full-length enriched, 15 days embryo whole body Mus

DEFINITION BY109350 musculus cDNA clone L330027E19 5', mRNA sequence.

ACCESSION BY109350

VERSION BY109350.1 GI:26219967

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 348)

AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gotohori, T., Baldarelli, R., Hill, D.P., Bul, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matzuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Brad, D., Brusic, V., Chocho, C., Corbani, L.E., Cousins, S., Della, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Giesi, C., Godzik, A., Gough, J., Grimmond, S., Guerinich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lemard, B., Lyons, P.A., Maglott, D.R., Maltale, L., Marchionni, L., McKenzia, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.D., Petrea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semp, C.A., Setou, M., Shimada, M., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

PUBMED 12466851

COMMENT

Contact: Yoshihide Hayashizaki
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 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
 Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Kono, H.,
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
 Shiraki, T., Tagami, M., Waki, K., Watanahki, A., Muramatsu, M. and
 Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.

FEATURES

source

Location/Qualifiers
 1..348
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="L330027E19"
 /tissue_type="whole body"
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 /clone_1ib="RIKEN full-length enriched, 15 days embryo
 whole body"

ORIGIN

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 Best Local Similarity 86.4%; Pred. No. 4.8e-35;
 Matches 184; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

1 ATGGTCTGAGTGGGCGCTGCTCCGAATGAAGAGCACTCGGCATTGAAGGCTTTAT 60
 Db ATGGTCTGAGTGGGCGCTGCTCCGAATGAAGAGCACTCGGCATTGAAGGCTTTAT 195
 61 CTGCATTAATATACAGCTTCTAGCTGAGAGGCTGCATGACGAGGAGGCTTTAAGGTGA 120
 Db CTGCACAAATATACAGCTTCTAGCTGAGAGGCTGCATGACGAGGAGGCTTTAAGGTGA 255
 121 GAGATCAGCGTGTCTCCCAATGCGTGGCTGATGCCAGCTGTCCCCGCTATCTGGGT 180
 Db GAGATCAGCGTGTCTCCCAATGCGTGGCTGATGCCAGCTGTCCCCGCTATCTGGGT 315
 256 GAGATCAGCGTGTCTCCCAATGCGTGGCTGATGCCAGCTGTCCCCGCTATCTGGGT 315
 181 GTCCAGGGGTGAAGCAGTGCCTGTCATGTGGG 213
 Db GTCCAGGGGTGAAGCAGTGCCTGTCATGTGGG 348

RESULT 24
 BY107750 343 bp mRNA linear EST 07-DEC-2002
 LOCUS BY107750
 DEFINITION Musculus cDNA clone L330014H07 5', mRNA sequence.
 ACCESSION BY107750
 VERSION BY107750.1 GI:26218367

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

EST.
 Mus musculus (house mouse)
 Mus musculus
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murinae; Mus.
 1 (bases 1 to 343)

TITLE

JOURNAL

PUBMED

COMMENT

Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
 Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Kono, H.,
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
 Shiraki, T., Tagami, M., Waki, K., Watanahki, A., Muramatsu, M. and
 Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.

FEATURES

source

Location/Qualifiers
 1..343
 /organism="Mus musculus"


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/mol_type="mRNA"  
/strain="C57BL/6J"  
/db_xref="taxon:10090"  
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ORIGIN

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Best Local Similarity 86.1%; Pred. No. 1.2e-33;  
Matches 179; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
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DB 136 ATGTCCTGAGTGGGCGCTGCTGCTTCCGAATGAAGGACTCGGCACTTGAAGTCTTAT 195  
   |||||  
OY 61 CTGCATTAATTAACCACTTCTAGCTGAGAGGGCTGCATGACAGGAGGAGTCAATTAAGTGA 120  
   |||||  
DB 196 CTGCATTAATTAACCACTTCTAGCTGAGAGGGCTGCATGACAGGAGGAGTCAATTAAGTGA 255  
   |||||  
OY 121 GAGATCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
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DB 256 GAGATCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 315  
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OY 181 GTTCAAGGCTGGAAGCCAGTGCCTGTCAT 208  
   |||||  
DB 316 GTTCAAGGCTGGAAGCCAGTGCCTGTCAT 343  
   |||||
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RESULT 25  
CK947864      689 bp      mRNA      linear      EST 15-MAR-2004  
LOCUS         4072568 BARC 10BOV Bos taurus cDNA clone 10BOV23_A09 5', mRNA  
DEFINITION  
ACCESSION  
CK947864  
VERSION  
CK947864.1 GI:45462244  
KEYWORDS  
EST.  
SOURCE  
ORGANISM  
Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 689)  
Sontegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay,  
G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.  
Production of EST from cDNA libraries derived from immunologically  
activated bovine gut  
unpublished (2004)  
Contact: Tad S. Sontegard  
Bovine Functional Genomics Laboratory  
Animal and Natural Resources Institute  
Bldg. 200 Rm2a BARC-East, Beltsville, MD 20705, USA  
Tel: 3015048416  
Fax: 3015048414  
Email: tade@anri.barc.usda.gov  
Single pass sequencing. Bases called and trimmed with phred  
0.000925 using options -trim alt -trim fasta. Vector identified  
by cross match using options -mismatch 12 -minscore 12  
Plate: 23 row: A column: 09  
Seq primer: CCCAGTCACGACCTGTGAACG  
High quality sequence stop: 689.  
Location/Qualifiers
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FEATURES  
source  
1..689  
/organism="Bos taurus"  
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/clone="10BOV23_A09"  
/sex="Male"  
/issue_type="Pooled"  
/dev_stage="Multiple"
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/lab_host="DH10B T1 phage resistant"  
/clone_lib="BARC 10BOV"  
/note="Organ: Small Intestine; Vector: pagen-1; Site 1:  
EcorV; Site 2: NotI; Equimolar amounts of mRNA extracted  
from proximal jejunums of 18 and 21 wk old steers, and  
distal ileums of 14 day old calves. Proximal jejunum  
exposed to C. oncophora for 3 and 6 weeks, and distal  
ileum exposed to C. parvum for 7 days"
```

ORIGIN

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Query Match      34.2%; Score 160; DB 7; Length 689;  
Best Local Similarity 76.6%; Pred. No. 3.7e-33;  
Matches 196; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
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OY 213 GGTGGGAGAGAGCGGACTTCAACACTAGAGCCAGTGAACATCATGAGCTTATCTTGG 272  
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DB 172 GAGAGCTTCAAGAGGGGAGAGGTCAATTAAGCCAGTAACATCATGAGCTTACACAG 231  
   |||||  
OY 273 TGCCAGGAATCCAAAGACTTCACTTCTACCGGCGGACATGGGGCTACCTCCAGCTT 332  
   |||||  
DB 232 TGCCAGGAAGCTTAAAAATTCACTTCTACCGGCGGACACGGGGCTCACCTCCAGCTT 291  
   |||||  
OY 333 CGAGTCGGCTGCTTACCGGCGCTGCTTCTGTGACAGGCTGCTGAAGCCGATCAGCTGT 392  
   |||||  
DB 292 TGAGTCGGCTGCTTACCGGCGCTGCTTCTGTGACAGGCTGCTGAAGCCGATCAGCTCT 351  
   |||||  
OY 393 CAGACTCACCGAGCTTCCCGGAATGTGGTGGAAATCCCGCATCAGACTTACTT 452  
   |||||  
DB 352 GCAGATCACCGAATCTCCGAAAGACACGAGCTGGACAAACCATCATGACTTACTT 411  
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OY 453 CCAGCAGTGTACTAG 468  
   |||||  
DB 412 CCAGCAGTGTACTAG 427  
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RESULT 26  
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LOCUS         4091856 BARC 10BOV Bos taurus cDNA clone 10BOV29_L23 5', mRNA  
DEFINITION  
ACCESSION  
CK952430  
VERSION  
CK952430.1 GI:45466810  
KEYWORDS  
EST.  
SOURCE  
ORGANISM  
Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 702)  
Sontegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay,  
G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.  
Production of EST from cDNA libraries derived from immunologically  
activated bovine gut  
unpublished (2004)  
Contact: Tad S. Sontegard  
Bovine Functional Genomics Laboratory  
Animal and Natural Resources Institute  
Bldg. 200 Rm2a BARC-East, Beltsville, MD 20705, USA  
Tel: 3015048416  
Fax: 3015048414  
Email: tade@anri.barc.usda.gov  
Single pass sequencing. Bases called and trimmed with phred  
0.000925 using options -trim alt -trim fasta. Vector identified  
by cross match using options -mismatch 12 -minscore 18  
Plate: 29 row: L column: 23  
Seq primer: CCCAGTCACGACCTGTGAACG  
High quality sequence stop: 702.  
Location/Qualifiers
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FEATURES  
source  
1..702  
/organism="Bos taurus"  
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/clone="10BOV29_L23"
/sex="Male"
/tissue_type="Pooled"
/dev_stage="Multiple"
/lab_host="DH10B T1 phage resistant"
/clone_lib="BARC 10BOV"
/note="Organ: Small intestine; Vector: pagen-1; Site: 1; EcorV; Site 2: NotI; Equimolar amounts of mRNA extracted from proximal jejunum of 18 and 21 wk old steers, and distal ileum of 14 day old calves. proximal jejunum exposed to C. oncophora for 3 and 6 weeks, and distal ileum exposed to C. parvum for 7 days"

ORIGIN

Query Match 34.2%; Score 160; DB 7; Length 702;
Best Local Similarity 76.6%; Pred. No. 3.8e-33;
Matches 16; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 213 GGTGGGGGAGAGCCGACTTAACTAGAGCCAGTACATCATGAGCTTATCTTG 272
DB 185 GGAGGCTTACAGCGGGAGAGCTATTAAAGCCAGTACATCATGAGCTTACACAG 244
QY 273 TGGCAAGAAATCCAGAGCTTCACTTTACCGCGGGACATGCGGCTCACTCCAGCTT 332
DB 245 TGGCGAGAAAGCTTAAATAATTCTTCTTCACTCGCGGGACACGCGGCTCACTCCAGCTT 304
QY 333 CAGATGGGCTGCTTACCGGGCTGGTTCCTGTGACAGGTCCTGAAGCCGATCAGCTGT 392
DB 305 TGAGTGGGCTGCTTACCGAGCTGGTTCCTGTGACAGGTCCTGAAGCTGACAGCTCT 364
QY 393 CAGACTCACCAGCTTCCGAGAAATGATGGTGGTGAATGCCCCCATCAGAGCTTACTT 452
DB 365 GCAGATCACCAGCTTCCGAGAAATGATGGTGGTGAATGCCCCCATCAGAGCTTACTT 424
QY 453 CCAGCAGTGTGACTAG 468
DB 425 CCAGCAATGTGACTAG 440

RESULT 27 689 bp mRNA linear EST 05-AUG-2004
CD368042
LOCUS UI-H-Ftl-bkc-a-09-0-UI.s1 NCI CGAP Ftl Homo sapiens cDNA clone
DEFINITION UI-H-Ftl-bkc-a-09-0-UI 3', mRNA sequence.
ACCESSION CD368042
VERSION CD368042.1 GI:31152132
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 689)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA sequence: 31-139, >LINE2 (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
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1..689
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/mol_type="mRNA"

/db xref="taxon:9606"
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/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Ftl"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; NCI-CGAP Ftl is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The RNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dF)18 tail. The sequence tag for this library is GGGCATGCGG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG TISSUE=Human Lung Alveolar Macrophage
TAG LIB=UI-H-Ftl
TAG_SEQ=GGCATGCGG"

ORIGIN

Query Match 32.7%; Score 153; DB 6; Length 689;
Best Local Similarity 100.0%; Pred. No. 3.3e-31;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 GGGCTCAGCTTCCAGCTTCAGTGGCTGCTTACCGGGCTGGTCTCTGTGACAGTGCT 375
DB 685 GGGCTCAGCTTCCAGCTTCAGTGGCTGCTTACCGGGCTGGTCTCTGTGACAGTGCT 626
QY 376 GAAGCCGATCAGCTTCTGACACTCACCGAGCTTCCGAGAAATGGTGGTGAATGCCCC 435
DB 625 GAAGCCGATCAGCTTCTGACACTCACCGAGCTTCCGAGAAATGGTGGTGAATGCCCC 566
QY 436 ATCAGAGCTTACTTCCAGAGGTGACTAG 468
DB 565 ATCAGAGCTTACTTCCAGAGGTGACTAG 533

RESULT 28 784 bp DNA linear GSS 17-JUN-2003
CC526753
LOCUS CH240_401P.T7 CHORI-240 Bos taurus genomic clone CH240_401P,
DEFINITION genomic survey sequence.
ACCESSION CC526753
VERSION CC526753.1 GI:31845041
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 784)

AUTHORS

Holt, R., Scott, J., Yang, G., Barber, S., Smailus, D., Prabh, A., L., Tsai, M., Cloutier, A., Lee, D., Ginn, N., Olson, T., Mayo, M., Butterfield, Y., Kirpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R., Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S., Schein, J., Maira, M., de Jong, P., Keefe, J. W. and Kappes, S. M. Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478 Unpublished (2003)
Other GSSs: CH240_401P1.TARBAC13P2
Contact: Rob Holt

TITLE
JOURNAL
COMMENT

Sequencing

The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
Tel: 604-877-6085
Fax: 604-877-6276
Email: rholtd@ccgsc.ca

Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering/information.html). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.
Plate: 401 row: P column: 1
Seq primer: T7
Class: BAC ends.

FEATURES

source

Location/Qualifiers
1..784

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/sex="Male"
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/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull LI Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 28.0%; Score 131; DB 9; Length 784;

Best Local Similarity 78.2%; Pred. No. 4.2e-25;
Matches 169; Conservative 0; Mismatches 46; Indels 1; Gaps 1;

253 ATCATGAGAGCTTATTTGGTGCAGAGATCCAGAGCTTACCTTACCGGGGGAC 312
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49 ATCATGAGAGCTTACCAACAGGCCGA-GAAGCTTACCTTACCTTACCGGGGGAC 107
|||
313 ATGGGGGCTACCTCCAGCTTGGAGTGGGCTTACCGGGGGCTGTCGTGACAGTG 372
|||
108 ACGGGGCTACCTCCAGCTTGGAGTGGGCTTACCGGGGGCTGTCGTGACAGTG 167
|||
373 CCTGAGCGGATCAGCTGTGACACTCACCAAGCTTCCGAGAGTGGTGGATGCC 432
|||
168 CCGAAGGCTGACAGCTCTGACAGATCACCAAGCTCCGAGAGACAGCTGGGCAAC 227
|||
433 CCCATACAGACTTCTACTTCCAGCAGTGTACTAG 468
|||
228 CCCATCATGAGCTTCTACTTCCAGCAGATGTACTAG 263
|||

RESULT 29

CF116914 501 bp mRNA linear EST 23-JUL-2003
LOCUS ad97.z1 ad adult sheep skin library Ovis aries CDNA, mRNA sequence.
DEFINITION CF116914
ACCESSION CF116914
VERSION CF116914.1 GI:33179328
KEYWORDS EST.
SOURCE Ovis aries (sheep)
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

REFERENCE
1 (bases 1 to 501)

Adelson, D.L., Cam, G. R., Desliya, U. and Franklin, I. R. Gene expression in sheep skin and wool (hair) JOURNAL Genomics 83 (1), 95-105 (2003)
Contact: Adelson, David L.
CSIRO Livestock Industries
306 Carmody Road, St Lucia QLD 4067, Australia
Tel: +61 7 3214 2700
Fax: +61 7 3214 2900
Email: li-enguiries@csiro.au.

FEATURES

source

Location/Qualifiers
1..501

/organism="Ovis aries"
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/strain="Merino"
/db_xref="taxon:9940"
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/clone_lib="ad adult sheep skin library"
/note="Organ: midflank skin; Vector: pTriplex; Site 1: EcoRI; Site 2: XbaI; Arrayed library filters screened by hybridization with labeled dinucleotide repeats. First strand synthesis XbaI-(dT)15 primed, EcoRI adaptors were ligated to cDNA before cloning. EcoRI-NotI-Sall adaptor sequence: 5'-AATTGGCGCGGTGAC GCGCGGAGACTG-PQ-5' sequencing primer 5' TACTACAGCTCATTACAGG 3' submitted sequences in excess of 50 bp after vector and quality clipping (phred 13) submitted to GenBank."

ORIGIN

Query Match 26.8%; Score 125.2; DB 6; Length 501;

Best Local Similarity 60.9%; Pred. No. 1.6e-23;
Matches 240; Conservative 0; Mismatches 148; Indels 6; Gaps 2;

15 GCGCGTGGCTTCCGATGAGAGAGCTCCGATTTGAGGTGCTTATCTGATATATACCA 74
|||
69 GCGAATAATCTACATATTAAGATGAGAGAGAGGCTCTGATCGTAGGAGTGCCA 128
|||
75 GCTTACCTGAGAGGCTGATGAGAGAGGATCTTAAAGTGAAGATCAGCGTGT 134
|||
129 GTTCTGTGGAGATCCGATGACAGACA--CTGTATGACAGACCATCTGATACT 185
|||
135 CCCCATGAGTGTGATGATGCAAGCTTCCCGCTCATCTGGGTGTCAGAGTGAAG 194
|||
186 CCCCAAGAGAGCTGGAACGACCAAGTCCCACTTCTTGGAGTCCAGAGGTAG 245
|||
195 CCAAGTCTGATGTGGGTTG---GGCAGAGAGCCGACTTAACTAGAGCCAGTGA 251
|||
246 CCGTGTCTGATGTGTGAGAGAGAGGAGGAGGCTTCCCTGAGAGTGAAGATGTGA 305
|||
252 CATCATGAGACTTATCTTGTGCGAAGATTCAGAGCTTACCTTACCGGCGGA 311
|||
306 CATGAGAGACCTGTCAAGAGGTGAGAGAAACACCCGCTTCACTTCTTCAAGAGA 365
|||
312 CATGGGCTCACCTCAGCTTGAAGTGGCTGACCCGGGCTGTCCTGACCGGT 371
|||
366 CTGAGGCCCGCTTTCAGGCTGAGGCTGCTGAGCTGAGCTGCTGCTCTCTGCTC 425
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372 GCGTGAAGCGATCAGCTGTGACATCACCGAG 405
|||
426 CTCTGACCCGACGAGCCCTGCACTTACCAAG 459
|||

RESULT 30

BY714015 621 bp mRNA linear EST 17-DEC-2002
LOCUS BY714015
DEFINITION BY714015 RIKEN full-length enriched, 0 day neonate skin Mus musculus CDNA clone 4632413N13 5', mRNA sequence.
ACCESSION BY714015
VERSION BY714015.1 GI:27126185

Tel: 86-1380-9770-743

Fax: 86-20-8775-4506

Email: yxzeng@zsunm.edu.cn.

FEATURES

source

Location/Qualifiers

FEATURES

source

Location/Qualifiers

1..593
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="human nasopharynx"
 /note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match 23.9%; Score 111.8; DB 6; Length 593;
 Best Local Similarity 59.1%; Pred. No. 8.3e-20;
 Matches 238; Conservative 0; Mismatches 147; Indels 18; Gaps 2;

24 CTTCCGATGGAAGAGCTGGCATTTGAGTGTATTCGATTAATACCACTTCTAGC 83
 141 CTTCCGATTTGGAGATTTAAACCAAGACCTTCTATCTGAGGAAACCACTAGTTC 200
 84 TGGAGGCTGATGAGGAGGATCAATTAAGTGAAGATCAGGTGTCCTCCAAATCG 143
 201 TGGATTAATTGAGAGGACCAATATGTCAATTTAGAGAGAAAGATAGATGTGTAACCATTTGA 260
 144 GTGGCTGATGCGACGCTTCCCGCTCATCTCGGTGTCCAGGGTGAAGCCATGCTT 203
 261 GCTCATATGCTC-----TGTCTTGGGAATCCATGAGGAGAGATGTGCTT 305
 204 GTCATGTGGGGT---GGGAGAGCCGACTCTAACACTAGAGCCAGTGAATCATGA 260
 306 GTCTGTGTCAGAGTCTGTGATGAGACCAAGATCCAGCTGAGGAGCATTAATCACTGA 365
 261 GCTCATATGTTGGTCCAGAGAAATCCAGAGCTTCACTTCAACCGGAGGAGATGGGCT 320
 366 CCTGAGCGAGAACAGAAACAGAGACAGAGGCTTCCGCTCATCCGCTCAGACAGGCGCC 425
 321 CACCTTCAGCTTCGAGTCCGCTGCCCTAACCAGGCTGCTTCTGTGACGGTCCCTGAAGC 380
 426 CACCAACAGATTTGAGTCTGCGCCCTGCGGCTGCTTCTGTGACAGCATGGAAGC 485
 381 CGATCAGCTGTGAGACTCAGCCAGGCTTCCGAGATGTGGC 423
 486 TGAACGCCCCGTACGCTTCAACCAATATGCTTGAAGAGCGTC 528

RESULT 32

BX416842

LOCUS

DEFINITION BX416842 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE001YA18

5-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 884)
 Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 15, 2003 this sequence version replaced gi:30763662.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

Location/Qualifiers

source

Location/Qualifiers

1..884
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DE001YA18"
 /issue_type="PLACENTA"
 /clone_lib="Homo sapiens PLACENTA"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match 23.6%; Score 110.6; DB 5; Length 884;
 Best Local Similarity 58.3%; Pred. No. 1.9e-19;
 Matches 235; Conservative 3; Mismatches 147; Indels 18; Gaps 2;

24 CTTCCGATGGAAGAGCTGGCATTTGAGTGTATTCGATTAATACCACTTCTAGC 83
 123 CTTCCGATTTGGAGATTTAAACCAAGACCTTCTATCTGAGGAAACCACTAGTTC 182
 84 TGGAGGCTGATGAGGAGGATCAATTAAGTGAAGATCAGGTGTCCTCCAAATCG 143
 183 CGGATTAATTGAGAGGACCAATATGTCAATTTAGAGAGAAAGATAGATGTGTAACCATTTGA 242
 144 GTGGCTGATGCGACGCTTCCCGCTCATCTCGGTGTCCAGGGTGAAGCCATGCTT 203
 243 GCTCATATGCTC-----CGCTGTCTTGGGAATCCATGAGGAGAGATGGGCTT 287
 204 GTCATGTG---GGTGGGAGAGAGCCGACTCTAACACTAGAGCCAGTGAATCATGA 260
 288 GCTGTGTGTCAGAGGCGGAGAGAGACCAAGATCCAGCKGAGGAGATTAATCACTGA 347
 261 GCTCATATGTTGGTCCAGAGAAATCCAGAGCTTCACTTCAACCGGAGGAGATGGGCT 320
 348 CCTGAGCGAGAACAGAAACAGAGACAGAGGCTTCCGCTCATCCGCTCAGACAGTGGCC 407
 321 CACCTTCAGCTTCGAGTCCGCTGCCCTAACCAGGCTGCTTCTGTGACGGTCCCTGAAGC 380
 408 CACCAACAGATTTGAGTCTGCGCCCTGCGGCTGCTTCTGTGACAGCATGGAAGC 467
 381 CGATCAGCTGTGAGACTCAGCCAGGCTTCCGAGATGTGGC 423
 468 TGAACGCCCCGTACGCTTCAACCAATATGCTTGAAGAGCGTC 510

RESULT 33

AY402945

LOCUS

DEFINITION AY402945 470 bp DNA linear GSS 15-DEC-2003

genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 470)
 Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
 Todd, M.A., Tanenbaum, D.M., Civiello, D.R., Lu, F., Murphy, B.,
 Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.V.,
 Adams, M.D. and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios

TITLE

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 470)

AUTHORS Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,

Todd, M.A., Tanenbaum, D.M., Civejlo, D.R., Lu, F., Murphy, B.,
 Ferriere, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
 Adams, M.D. and Cargill, M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA

COMMENT
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

FEATURES
 source
 1..470
 Location/Qualifiers

gene
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 <1..>470
 /gene="IL1RN"
 /locus_tag="HCM1393"

ORIGIN

Query Match 23.5%; Score 110.2; DB 10; Length 470;
 Best Local Similarity 58.8%; Pred. No. 2.2e-19;
 Matches 237; Conservative 0; Mismatches 148; Indels 18; Gaps 2;

```

QY 24 CTTCCGAATGAAAGACTCGGCAATGAGGTCTTATCTGCATTAATACCAAGCTTCTAGC 83
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 47 CTTCAAGAACTGGAGTGTTAACCAAGAACTCTATCTAGAGAACACCAACTAGTTGC 106
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 84 TGGAGGGCTGCATGACGAGGAGTCAATTAAGTGAAGATCAGGTGTGCCCCCAATG 143
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 107 TGGATACCTTGCAAGAGCCAAATGTCAATTAAGAAAGAAATGATGATGTGATCCCAATTA 166
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 144 GTGGCTGATGACAGGCTGTCCCGCTCATCTCGGTGTCCAGGGTGAAGCCAGTGCCT 203
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 167 GCCTCATGCTC-----TGTTCTTGGGAATTCATGAGGGAAGATGTGCTT 211
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 204 GTCATGTGGGGTG---GGCAGAGCCGACTTAACACTAGAGCCGTAACATCATGGA 260
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 212 GTCTGTGTCAAGTGTGTGATGAGACAGACTCCAGCTGAGGCGATTAACTCACTGA 271
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 261 GCTCATCTTGGTCCCAAGAAATCCAAAGCTTCACTTCACTCCGCGGGAATGGGGCT 320
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 272 CTTGAGCGAAGAACAGAAACAGACAGAGCTTGGCTTATCCGCTCAGACAGTGGCC 331
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 331 CACCTTCAGCTTGAAGTCCGCTGCTACCCGGGCTGTTCTGTGACCGGTCTGAAGC 380
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 332 CACCAACCACTTTTGAAGTCTGCCGCTGCCCGGTTGGTTCCTTGACACGCAATGGAAGC 391
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 381 CGATCAGCTGTGACATCAGCCAGCTTCCGAGAAATGATGATG 423
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 392 TGACCAAGCCCGTCAAGCTCACCATAATGCTGACGAAAGCGTC 434
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 34
 CR994825 615 bp mRNA linear EST 28-JUN-2005
 LOCUS CR994825 RZPD no. 9016 Homo sapiens cDNA clone RZPD9016N0622 5',
 DEFINITION mRNA sequence.
 ACCESSION CR994825
 VERSION CR994825.1 GI:68288710
 KEYWORDS EST.
 SOURCE
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 615)
 Heil, O., Ebert, L., Hennig, S., Henze, S., Radelof, U., Schneider, D.
 and Korn, B.
 Human T-Lymphocytes Library
 TITLE Human T-Lymphocytes Library
 JOURNAL Unpublished (2005)
 COMMENT
 CONTACT: Inge Airlart
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Email: www.rzpd.de

RZPD: RZPD9016N0622.

RZPDLIB: (Human T-Lymphocytes) RZPD LIB No. 9016
<http://www.rzpd.de/cgi-bin/products/set.cgi?libno=9016> Contact:

Inge Airlart
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 100
 Fax: +49 30 32639 111
 www.rzpd.de

This clone is available from RZPD:
<http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=RZPD9016N0622>
 contact RZPD (product - support@rzpd.de) for further information.
 Primer name: qe3 4, Primer sequence: CGGATTAACAATTCACACAG.

FEATURES
 source
 Location/Qualifiers

1..615
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="RZPD9016N0622"
 /rname="RZPD9016N0622"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_1ib="RZPD no. 9016"
 /note="Vector: pQE80LSN_cloned; site_1: SalI; site_2:
 NotI; vector:
http://www.rzpd.de/info/vectors/pQE80LSN_cloned.pic.shtml
 ; 1st strand cDNA was prepared from mRNA obtained from
 human T-Lymphocytes with a NotI - oligo (dt) primer [5'
 GACTGCTTCAATGCTGCGAGCGCGCCCTTTTCTTTTCTTTT 3']
 Double-stranded cDNA was ligated to SalI adaptor,
 digested with NotI and cloned into the NotI and SalI sites
 of the pQE80LSN_cloned vector"

ORIGIN

Query Match 23.5%; Score 110.2; DB 7; Length 615;
 Best Local Similarity 58.8%; Pred. No. 2.3e-19;
 Matches 237; Conservative 0; Mismatches 148; Indels 18; Gaps 2;

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QY 24 CTTCCGAATGAAAGACTCGGCAATGAGGTCTTATCTGCATTAATACCAAGCTTCTAGC 83
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 102 CTTCAAGAACTGGAGTGTTAACCAAGAACTCTATCTAGAGAACACCAACTAGTTGC 161
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 84 TGGAGGGCTGCATGACGAGGAGTCAATTAAGTGAAGATCAGGTGTGCCCCCAATG 143
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 162 TGGATACCTTGCAAGAGCCAAATGTCAATTAAGAAAGAAATGATGATGTGATCCCAATTA 221
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 144 GTGGCTGATGACAGGCTGTCCCGCTCATCTCGGTGTCCAGGGTGAAGCCAGTGCCT 203
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 222 GCCTCATGCTC-----TGTTCTTGGGAATTCATGAGGGAAGATGTGCTT 266
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 204 GTCATGTGGGGTG---GGCAGAGCCGACTTAACACTAGAGCCGTAACATCATGGA 260
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 267 GTCTGTGTCAAGTGTGTGATGAGACAGACTCCAGCTGAGGCGATTAACTCACTGA 326
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 261 GCTCATCTTGGTCCCAAGAAATCCAAAGCTTCACTTCACTCCGCGGGAATGGGGCT 320
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 327 CTTGAGCGAAGAACAGAAACAGACAGAGCTTGGCTTATCCGCTCAGACAGTGGCC 386
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 331 CACCTTCAGCTTGAAGTCCGCTGCTACCCGGGCTGTTCTGTGACCGGTCTGAAGC 380
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 387 CACCAACCACTTTTGAAGTCTGCCGCTGCCCGGTTGGTTCCTTGACACGCAATGGAAGC 446
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 381 CGATCAGCTGTGACATCAGCCAGCTTCCGAGAAATGATGATG 423
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 447 TGACCAAGCCCGTCAAGCTCACCATAATGCTGACGAAAGCGTC 489
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 35
 BI489807 864 bp mRNA linear EST 28-AUG-2001
 LOCUS BI489807 603031536P1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5172896 5',
 DEFINITION mRNA sequence.
 ACCESSION BI489807

```

VERSION      BI489807.1  GI:15329035
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homiidae; Homo.
REFERENCE    1 (bases 1 to 864)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabs-rt@mail.nih.gov
              Tissue Procurement: Life Technologies, Inc.
              cDNA Library Preparation: Life Technologies, Inc.
              DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LNL at:
              http://image.llnl.gov
              Place: LBL/LL1430 row: 9 column: 09
              High quality sequence stop: 862.
              Location/Qualifiers
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                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:5172896"
                /lab_host="DH10B"
                /clone_1ib="NIH MGC 115"
                /note="Organ: pooled brain, lung, testis; Vector:
                pCMV-Sport6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
                source anonymous pool of 6 male brains, age range 23-27; 1
                male lung, age 27; and 1 male testis, age 69. Library is
                oligo-dT primed and directionally cloned (EcoRV site is
                destroyed upon cloning). Average insert size 1.8 kb,
                insert size range 1-3 kb. Library is normalized and
                enriched for full-length clones and was constructed by C.
                Gruber (Invitrogen). Research Genetics tracking code
                021. Note: this is a NIH MGC Library."

ORIGIN
Query Match      23.5%; Score 110.2; DB 3; Length 864;
Best Local Similarity 58.8%; Pred. No. 2.5e-19;
Matches 237; Conservative 0; Mismatches 148; Indels 18; Gaps 2;

QY 24 CTTCCGAATGAAGACTCGGCAATTGAAGTCTTATCTGCATATATACCAAGCTTCTAGC 83
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 144 CTTCAAGATCTGGAGATTAAACAGAAAGCTTCTATCTGAGGAAACAACCACTAGTTGC 203
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 84 TGAAGGGCTGCATGCAGGGAAGGTCAATTAAGGTGAAGATCAGGTGTCCTCCCAATGC 143
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 204 TGGATATCTTGCAAGGACCAATGTCAATTAAGAAAGAAATGATGTGTATCCCAATTA 263
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 144 GTGGCTGATGTCAGAGCTGTCCCGTCATCTCGGGTGTCCAGGGTGAAGCCAGTGCCT 203
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 264 GCGTCATGCTC-----TGTTCTTGGGAATCCATGAGGGAAGATGTGGCT 308
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 204 GTTCATGTGGGGTG---GGGACAGAGCCGACTTAACTAGAGCCAGTAACATCTATGA 260
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 309 GTTCCTGTGTCAGTCTGTGATGAGACAGACTCCAGTGAAGGACAGTTAACTATCACTGA 368
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 261 GCTCTATCTTGGTGCAGGAATCCAAAGCTTCACTTCAACCGCGGGAACATGTGGGCT 320
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 369 CCTGAGCGAAGAACAGAAAGAGAGCAAGCGCTTCCGCTTCATCCGTCAGACAGCGGCC 428
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QY 321 CACCTCAAGCTTGAAGTGGGCTGCTAACCCGGGCTGGTTCCTGTGACGGTGCCTGAAGC 380
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 429 CACCAACAAGTTTGAATCTGCGGCTGCGCCGGTGGTTCCTGTGACAGCAGATGAAGC 488
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 381 CGATCAGCCTGTGAGACTCAACCAAGCTTCCGGAATGTGGC 423
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 489 TGAACAGCCGCTCAGCCTCAATATGCTGACGAAGGCGTC 531
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 36
C619093
LOCUS
DEFINITION C619093 1581 bp mRNA linear HTC 21-JUL-2004
            full-length cDNA clone CSOD1086VA15 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   C619093
VERSION     C619093.1  GI:50499900
KEYWORDS    HTC; CDSUT_cDNA
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homiidae; Homo.
REFERENCE    1 (bases 1 to 1581)
AUTHORS      Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE        Full-length cDNA libraries and normalization
JOURNAL      Unpublished
COMMENT      Contact : Feng Jiang Email : fjiang@lifetech.com URL :
              http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
              Faraday Avenue
              2 (bases 1 to 1581)
              Genoscope.
REFERENCE    Direct Submission
AUTHORS      Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
TITLE        BP 191 91006 EVRY cedex - FRANCE (E-mail : segreg@genoscope.cns.fr
              - Web : www.genoscope.cns.fr)
              1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
              end enriched, double-strand cDNA was digested with Not I and cloned
              into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
              was normalized. Library was constructed by Life Technologies, a
              division of Invitrogen.
              Location/Qualifiers
                1..1581
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="CSOD1086VA15"
                /tissue_type="Placenta Cot 25-normalized"
                /plasmid="pCMVSPORT_6"

ORIGIN
Query Match      23.5%; Score 110.2; DB 4; Length 1581;
Best Local Similarity 58.8%; Pred. No. 2.8e-19;
Matches 237; Conservative 0; Mismatches 148; Indels 18; Gaps 2;

QY 24 CTTCCGAATGAAGACTCGGCAATTGAAGTCTTATCTGCATATATACCAAGCTTCTAGC 83
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 48 CTTCAAGATCTGGAGATTAAACAGAAAGCTTCTATCTGAGGAAACAACCACTAGTTGC 107
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 84 TGAAGGGCTGCATGCAGGGAAGGTCAATTAAGGTGAAGATCAGGTGTCCTCCCAATGC 143
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 108 TGGATATCTTGCAAGGACCAATGTCAATTAAGAAAGAAATGATGTGTATCCCAATTA 167
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 144 GTGGCTGATGTCAGAGCTGTCCCGTCATCTCGGGTGTCCAGGGTGAAGCCAGTGCCT 203
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 168 GCGTCATGCTC-----TGTTCTTGGGAATCCATGAGGGAAGATGTGGCT 212
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 204 GTTCATGTGGGGTG---GGGACAGAGCCGACTTAACTAGAGCCAGTAACATCTATGA 260
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 213 GTTCGTGTGTCAGTCTGTGATGAGACAGACTCCAGTGAAGGACAGTTAACTATCACTGA 272
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 261 GCTCTATCTTGGTGCAGGAATCCAAAGCTTCACTTCAACCGCGGGAACATGTGGGCT 320
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 273 CCTGAGCGAAGAACAGAAAGAGAGCAAGCGCTTCCGCTTCATCCGTCAGACAGTGGGCC 332
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 321 CACCTCAAGCTTGAAGTGGGCTGCTAACCCGGGCTGGTTCCTGTGACGGTGCCTGAAGC 380
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 333 CACCAACAAGTTTGAATCTGCGGCTGCGCCGGTGGTTCCTGTGACAGCAGATGAAGC 392
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 381 CGATCAGCCTGTGAGACTCAACCAAGCTTCCGGAATGTGGC 423
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 393 TGACGAGCCGTCAGCCTACCAATATGCTGAGGAGCGTC 435

RESULT 37
LOCUS CR616671 1644 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DM013YE17 of Fetal liver of Homo sapiens (human).
ACCESSION CR616671
VERSION CR616671.1 GI:50497478
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1644)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue
2 (bases 1 to 1644)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
Location/Qualifiers
1. .1644
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM013YE17"
/issue_type="Fetal liver"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 23.5%; Score 110.2; DB 4; Length 1644;
Best Local Similarity 58.8%; Pred. No. 2,8e-19;
Matches 237; Conservative 0; Mismatches 148; Indels 18; Gaps 2;

24 CTTCCGATGAGGACTCGGCAATTGAAGGCTTTATCTGCATTAATACCAAGCTTACG 83
118 CTTGAGAACTCTGGAGATTAAACGAAAGACCTTCTATCTGAGGAAACCACTTAAGTGC 177
84 TGGAGGCTGTCATGACGAGGAGGTCATTAAGGTGAAGATCAGCGTGTCCCAATCG 143
178 TGGATCTTGCAGGACCAAAATGTCAATTAGAAAGAAAGATGATGTGGTACCAATGGA 237
144 GTGGCTGATGCGACGCTGTCCCGCTCATCTGGGTGTCAGGGGTGAAGCAAGTGCCT 203
238 GCGTCATGCTC-----TGTCTTGGGAATCCATGAGGGGAAGATGTGCTT 282
204 GTCATGTGGGGTNG---GGGAGAGCGGCACTTAACATAGAGCCAGTGAACATCATGGA 260
283 GTCTGTGTCAAGTCTGTGATGATGACACAGATCCAGCTGAGGAGGATTAACATCACTGA 342
261 GCTTATCTTGTGTCAGGAATCCAAAGCTTCACTTCTTACCGGCGGAGCAATGGGGCT 320
343 CCGAGCGAGAACAGAAAGAGAGGAGCAAGGCGCTTCGCTTCATCGCTCAGACAGTGGCCC 402
321 CACTTCAGCTTGAATCGGCTGCTTACCGGGCTGTCTCTGTGACAGGTGCTGAAGC 380
403 CACCAACAAATTTGATGTGCGCGCTGCCCGGTGGTTCCTTGCACAGCGATGGAAGC 462
381 CGATCAGCTGTGAGCTACCAAGGCTTCGCGGATGTGAGC 423

Db 463 TGACGAGCCGTCAGCCTACCAATATGCTGAGGAGCGTC 505

RESULT 38
LOCUS CR605915 1666 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DE01YAL7 of Placenta of Homo sapiens (human).
ACCESSION CR605915
VERSION CR605915.1 GI:50486722
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1666)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue
2 (bases 1 to 1666)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
Location/Qualifiers
1. .1666
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE01YAL7"
/issue_type="Placenta"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 23.5%; Score 110.2; DB 4; Length 1666;
Best Local Similarity 58.8%; Pred. No. 2,8e-19;
Matches 237; Conservative 0; Mismatches 148; Indels 18; Gaps 2;

24 CTTCCGATGAGGACTCGGCAATTGAAGGCTTTATCTGCATTAATACCAAGCTTACG 83
123 CTTGAGAACTCTGGAGATTAAACGAAAGACCTTCTATCTGAGGAAACCACTTAAGTGC 182
84 TGGAGGCTGTCATGACGAGGAGGTCATTAAGGTGAAGATCAGCGTGTCCCAATCG 143
183 TGGATCTTGCAGGACCAAAATGTCAATTAGAAAGAAAGATGATGTGGTACCAATGGA 242
144 GTGGCTGATGCGACGCTGTCCCGCTCATCTGGGTGTCAGGGGTGAAGCAAGTGCCT 203
243 GCGTCATGCTC-----TGTCTTGGGAATCCATGAGGGGAAGATGTGCTT 287
204 GTCATGTGGGGTNG---GGGAGAGCGGCACTTAACATAGAGCCAGTGAACATCATGGA 260
288 GTCTGTGTCAAGTCTGTGATGATGACACAGATCCAGCTGAGGAGGATTAACATCACTGA 347
261 GCTTATCTTGTGTCAGGAATCCAAAGCTTCACTTCTTACCGGCGGAGCAATGGGGCT 320
348 CCGAGCGAGAACAGAAAGAGAGGAGCAAGGCGCTTCGCTTCATCGCTCAGACAGTGGCCC 407
321 CACTTCAGCTTGAATCGGCTGCTTACCGGGCTGTCTCTGTGACAGGTGCTGAAGC 380
408 CACCAACAAATTTGATGTGCGCGCTGCCCGGTGGTTCCTTGCACAGCGATGGAAGC 467

QY 381 CGATAGCCTGTGACACTCACCACCTTCCCGAGAAATGTGTC 423
 DB 468 TGACACGCCCTGACCTCACCATAATGCTGACGAGGCTC 510
 RESULT 39
 CD468528 735 bp mRNA linear EST 04-JUN-2003
 LOCUS Leukos3_3.D10.g1.A025 Stimulated peripheral blood leukocytes S3
 DEFINITION Equus caballus cDNA clone Leukos3_3.D10.A025 5', mRNA sequence.
 ACCESSION CD468528
 VERSION CD468528.1 GI:31389796
 KEYWORDS EST
 SOURCE Equus caballus (horse)
 ORGANISM Equus caballus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
 Vandenplas, M., Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S.,
 Moore, J.N., Liang, C., Sun, F., Sullivan, R., Shah, M. and Pratt, L.H.
 An EST database from equine (Equus caballus) stimulated peripheral
 blood leukocytes
 Unpublished (2003)
 JOURNAL Contact: Cordonnier-Pratt MM
 COMMENT Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Km. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmprratt@uga.edu
 Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
 the Human Genome Center, University of Tokyo Institute of Medical
 Science; tissue and RNA were prepared in the Department of Large
 Animal Medicine, University of Georgia; sequencing done in the
 Laboratory for Genomics and Bioinformatics, University of Georgia.
 Sequence ends have been trimmed to exclude vector and regions below
 phred quality 16. Three-prime sequences are presented as their
 reverse complement and have been trimmed to exclude polyA.
 Seq primer: Sugs (CTCTGCTTAAAGCTGCG).
 Location/Qualifiers
 1..735
 /organism="Equus caballus"
 /mol_type="mRNA"
 /strain="Tennessee walking horse"
 /db_xref="taxon:9796"
 /clone="Leukos3_3.D10.A025"
 /sex="female"
 /tissue_type="blood"
 /cell_type="leukocytes"
 /lab_host="DH10B-T1 phage-resistant E. coli"
 /clone_lib="Stimulated peripheral blood leukocytes S3"
 /note="Organ: circulatory system; Vector: pME18S-FL3;
 Site 1: XhoI; Site 2: XhoI; The library was prepared from
 polyA+ RNA from equine peripheral blood leukocytes
 isolated from a healthy adult horse. The leukocytes were
 stimulated for 4 hr with 10 ng/ml E. coli O55:B5 LPS.
 Double-stranded cDNA was cloned unidirectionally into
 different DraIII sites of the pME18S-FL3 vector (5-prime
 DraIII site is CACTGTGTG, 3-prime DraIII site is
 CACCATGTG). XhoI excises the cDNA insert."

ORIGIN
 Query Match 23.3%; Score 109; DB 6; Length 735;
 Best Local Similarity 57.0%; Pred. No. 5.2e-19;
 Matches 249; Conservative 0; Mismatches 170; Indels 18; Gaps 2;

QY 24 CTTCCAAATGAGGACTCGGCAATTTGCGCTTATCGCATTAATACAGCTTCAGC 83
 DB 141 CTTCAAGATTTGGAGATTATACCAAGACCTTCTACATATGAGAAATACCACTAGTGC 200
 QY 84 TGGAGGCGCTGCATATCAGGAGGATCTTAAGGTGAAGATCAGCGTGTCCCAATGC 143
 DB 201 TGGATATCTTGCAGAAATCAAAATCTAAATTAACAAGAGAAATATGTTGTGTGCCCATTTGA 260

QY 144 GTGGCTGAGTGCAGCCGTGTCCTCCCGTATCTGGGTGTCCAGGGTGAAGCCAGTGCCT 203
 DB 261 G-----CTGATGCTCTATTCTCTGGGAATCTCATGGAGAGAGCTGTGCT 305
 QY 204 GTCATGTG---GGTGGGGCAGAGCCGACTTAACACTAGAGCCAGTAACTATGGA 260
 DB 306 GGCCTGTGTAAGTCTGTGATGAGATTAGGTCCAAATTGAGCAGATTAACTACATGA 365
 QY 261 GCTTATCTTGGTGGCAAGAAATCCAGAGCTTCACTTCAACGGCGGAGCATGGGGCT 320
 DB 366 CCTGAGCAAGAACAAAGAGGAGAAACAGCGCTTCACTTCAATCCGCTCAAAACATGGGCC 425
 QY 321 CACCTCGAGCTTGAAGTGGCTGCTTACCCGGGCTGTTCCTGTGTCACAGGTGCTGAAGC 380
 DB 426 CACCAACGAGCTTCAGATGTGCGCGCTGCTGCGCTGTCTCTCTCAACGGCGCGGAGGC 485
 QY 381 CGATCAGCCTGTGACACTCACCAGCTTCCGAGAAATGTGGTGAATGCCCATCAC 440
 DB 486 AGACGGCCTGTGACGCTCACCACCAAGCCCTCAGAAAGAGGTACACGACCTCGTAAC 545
 QY 441 AGACTTCTACTTCCAGC 457
 DB 546 AGACTCTGTCTCCAGC 562

RESULT 40
 LOCUS CV027812 572 bp mRNA linear EST 20-AUG-2004
 DEFINITION 6164 Full Length cDNA from the Mammalian Gene Collection Homo
 sapiens cDNA 5' similar to BC009745, mRNA sequence.
 ACCESSION CV027812
 VERSION CV027812.1 GI:51485880
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1..572
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="mixed"
 /clone_lib="Full Length cDNA from the Mammalian Gene

REFERENCE
 AUTHORS Rual, J.F., Hirozane-Kishikawa, T., Hao, T., Bertin, N., Li, S.,
 Dricot, A., Li, N., Rosenberg, J., Lamesch, P., Vidalain, P.O.,
 Clingingsmith, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T.,
 Simmons, B., Segueria, R., Bosak, S., Doucette-Stamm, L., Le Peuch, C.,
 Vandenhaute, J., Cusick, M.E., Albaladejo, J.S., Hill, D.E. and Vidal, M.
 Human ORFome Version 1.1: a Platform for Reverse Proteomics
 Genome Res. (2004) In press
 JOURNAL
 COMMENT
 TITLE Marc Vidal Laboratory
 Dana Farber Cancer Institute
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 5739
 Email: Marc_Vidal@dfci.harvard.edu
 ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
 results from a PCR reaction using an MGC full-length cDNA as
 template DNA and ORF specific primers
 PCR Primers
 FORWARD: ATGGCTTTAGAGCATCTG
 BACKWARD: TACTGCTCTCTGTAAGTAGAA
 Insert Length: 572 Std Error: 28.00
 Plate: 11002 row: 07 column: G
 Seq primer: ACTGGCGCGTGTTCACAGCGTGTACTGGGAAAC
 High quality sequence start: 100
 High quality sequence stop: 571
 POLYA=NO.

FEATURES
 source Location/Qualifiers
 1..572
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="mixed"
 /clone_lib="Full Length cDNA from the Mammalian Gene

Collection"
/note="Vector: mixed; The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR223 Donor vector. Reference: MGC (Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Full-length Human and Mouse cDNA Sequences. PNAS, 2002, 99(126), 16899-16903"

Query Match 23.2%; Score 108.6; DB 7; Length 572;
Best Local Similarity 58.6%; Pred. No. 6.3e-19;
Matches 236; Conservative 0; Mismatches 149; Indels 18; Gaps 2;

FEATURES
source Location/Qualifiers
1..757
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS00001Y17"
/issue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN
Query Match 23.2%; Score 108.6; DB 7; Length 572;
Best Local Similarity 58.6%; Pred. No. 6.3e-19;
Matches 236; Conservative 0; Mismatches 149; Indels 18; Gaps 2;
24 CTTCCGAATGAGAGCTCGGCACTTGAAGTGTCTTATCTGCATTAATACCACTTTACG 83
57 CTTCCGAATCTGGAGATGTTAAACCAAGACCTTCTATCTGAGAGAACCACTAGTTCG 116
84 TGGAGGGCTGTCAGTGCAGGAGAGTCAATTAAGGTGAAGATCAGCGTCCCAATCG 143
117 CGGATACCTTGCAGAGACCAATATGTCAATTAGAGAAAGATAGATGTGTACCAATGA 176
144 GTGGCTGATGTCAGACCTCTCCCGCTCATCTCGGTGTCCAGGGTGAAGCCAGTGCCT 203
177 GCCTCATGCTC-----TGTCTTGGGAATCCATGAGGAGGAAGATGTGCCT 221
204 GTCATGTGGGGTG---GGCAGAGCCGCACTTAACATAGAGCCAGTGAACATCATGA 260
222 GTCTGTGTCAAGTGTGATGATGAGACAGACTCCAGCTGAGAGCGATTAAATCATCTGA 281
261 GCTCTATCTTGGTGCCAGAAATCCAGAGCTTCACTTACCGCGGAGACATGGGGCT 320
282 CCTGAGCCAGAACAGAAACAGAGACAGAGGCTTCGCTTATCCGTCAGACAGATGGCCC 341
321 CACCTTCAGCTTGAAGTGGCTGCTTACCCGGGCTGTCTGTGACAGGTCCTGAAGC 380
342 CACCAACAGTTTGTAGTGTGCGCGCTGCGCGGTTGTCTCTGTGACAGCATGGAAGC 401
361 CGATCAGCTGTGACAGCTACCCAGCTTCCGAGATGTGGC 423
402 TGACCAAGCCGTCACGCTCACCAATATGCTGACAGAGGCGTC 444

RESULT 41
BX424058 757 bp mRNA linear EST 01-MAY-2004
DEFINITION BX424058 Homo sapiens PLACENTA Homo sapiens cDNA clone CS00001Y17
5-PRIME, mRNA sequence.
BX424058
ACCESSION BX424058.2 GI:46928937
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 757)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30647665.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by life technologies, a
division of invitrogen.
This sequence belongs to sequence cluster 138.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS1DE0012A06QPlac=138.f.

ORIGIN
Query Match 23.2%; Score 108.6; DB 5; Length 757;
Best Local Similarity 58.6%; Pred. No. 6.7e-19;
Matches 236; Conservative 0; Mismatches 149; Indels 18; Gaps 2;
24 CTTCCGAATGAGAGCTCGGCACTTGAAGTGTCTTATCTGCATTAATACCACTTTACG 83
123 CTTCCGAATCTGGAGATGTTAAACCAAGACCTTCTATCTGAGAGAACCACTAGTTCG 182
84 TGGAGGGCTGTCAGTGCAGGAGAGTCAATTAAGGTGAAGATCAGCGTCCCAATCG 143
183 CGGATACCTTGCAGAGACCAATATGTCAATTAGAGAAAGATAGATGTGTACCAATGA 242
144 GTGGCTGATGTCAGACCTCTCCCGCTCATCTCGGTGTCCAGGGTGAAGCCAGTGCCT 203
243 GCCTCATGCTC-----TGTCTTGGGAATCCATGAGGAGGAAGATGTGCCT 287
204 GTCATGTGGGGTG---GGCAGAGCCGCACTTAACATAGAGCCAGTGAACATCATGA 260
288 GTCTGTGTCAAGTGTGATGATGAGACAGACTCCAGCTGAGAGCGATTAAATCATCTGA 347
261 GCTCTATCTTGGTGCCAGAAATCCAGAGCTTCACTTACCGCGGAGACATGGGGCT 320
348 CCTGAGCCAGAACAGAAACAGAGACAGAGGCTTCGCTTATCCGTCAGACAGATGGCCC 407
321 CACCTTCAGCTTGAAGTGGCTGCTTACCCGGGCTGTCTGTGACAGGTCCTGAAGC 380
408 CACCAACAGTTTGTAGTGTGCGCGCTGCGCGGTTGTCTCTGTGACAGCATGGAAGC 467
361 CGATCAGCTGTGACAGCTACCCAGCTTCCGAGATGTGGC 423
468 TGACCAAGCCGTCACGCTCACCAATATGCTGACAGAGGCGTC 510

RESULT 42
BX406656 932 bp mRNA linear EST 01-MAY-2004
DEFINITION BX406656 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
CS00M013Y17 5-PRIME, mRNA sequence.
BX406656
ACCESSION BX406656.2 GI:46926367
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 932)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30639467.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1388.f. For more information about this cluster, see <http://www.genoscope.cns.fr/cdna28=CS0AM013AC09QPl&c=1388.f>.

FEATURES

source

Location/Qualifiers

1..932

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DM013YE17"

/tissue_type="FETAL LIVER"

/dev_stage="fetal"

/clone_lib="Homo sapiens FETAL LIVER"

/note="Organ: Liver; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NciI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match 23.2%; Score 108.6; DB 5; Length 932;

Best Local Similarity 58.6%; Pred. No. 7e-19;

Matches 236; Conservative 0; Mismatches 149; Indels 18; Gaps 2;

```

24 CTTCCGAATGAAAGACTGGCATTTGAAGTCTTATCTGCAATTAATACCACTTCTAGC 83
118 CTTTCAAGATCTGGGATGTTTACCAAGAACCTTTCTATCTGAGAACCAACCACTAGTGC 177
84 TGGAGGGCTGCATGACGAGGAGATCAATTAAGTGAAGATCAGCGTGTCCCAATCG 143
178 CGGATACCTTGCAAGACCAATCTCAATTTAAGAAAGATAGATGTGTACCATTTGA 237
144 GTGGTGAATGCCAGCTGTCTCCCGTCATCTTGGGTGTCCAGGGTGAAGCCAGTGCCT 203
238 GCCTCATGTCTC-----TGTTCTTGGGAATCCATGGAGGGAGATGTGCTT 282
204 GTCATGTGGGGT---GGGACAGAGCCGACTCTTAACATGAGCCAGTGAATCATGGA 260
283 GTCTGTGTCAAGTCTGTGATGACACAGACTCCAGCTGAGGACGTTAATCATCTGA 342
261 GCTCTATCTTGGTGCCAAAGATCCAAAGACTTCACTTCAACCGCGGAGATGGGGCT 320
343 CTTGAGCGGAGAACAAAGACGAGACGAGGCTTCCGCTTATCCGTCAGACAGTGGCCC 402
321 CACCTTCAGCTTGAAGTGGCTGCTTACCCGCGGCTGTCTGTGCAAGCGTGCCTGAAGC 380
403 CACCAACAGTTTGAAGTGTGCGCGCTGCGCCGTTGTCTCTGCAACAGCATGGAGAC 462
381 CGATCAGCTGTGACATCAACCCAGCTTCCGAGATGGTGGC 423
463 TGACCAGCCCGTCAAGCTTCAACCAATATGCTTGAAGAGCGTGC 505

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RESULT 43

BE563703 938 bp mRNA linear EST 15-AUG-2000

LOCUS 60135333F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689284 5',

DEFINITION mRNA sequence.

ACCESSION BE563703

VERSION BE563703.1 GI:9807423

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

1 (bases 1 to 938)

NIH-MGC <http://mgi.nci.nih.gov/>.

Unpublished (1999)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

JOURNAL COMMENT

Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
Plate: L1CM383 row: n column: 05
High quality sequence stop: 764.

FEATURES

source

Location/Qualifiers

1..938

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3689284"

/tissue_type="adenocarcinoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: pancreas; Vector: pOTB7, Site 1: XhoI, Site 2: EcoRI; cDNA made by oligo-dT priming.

directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACAG(G) library constructed

by Ling Hong in the Laboratory of Gerald M. Rubin

(University of California, Berkeley) using ZAP-cDNA

synthesis kit (Stratagene) and Superscript II RT (Life

Technologies)."

ORIGIN

Query Match 23.2%; Score 108.6; DB 2; Length 938;

Best Local Similarity 58.6%; Pred. No. 7e-19;

Matches 236; Conservative 0; Mismatches 149; Indels 18; Gaps 2;

```

24 CTTCCGAATGAAAGACTGGCATTTGAAGTCTTATCTGCAATTAATACCACTTCTAGC 83
67 CTTTCAAGATCTGGGATGTTTACCAAGAACCTTTCTATCTGAGAACCAACCACTAGTGC 126
84 TGGAGGGCTGCATGACGAGGAGATCAATTAAGTGAAGATCAGCGTGTCCCAATCG 143
127 CGGATACCTTGCAAGACCAATCTCAATTTAAGAAAGATAGATGTGTACCATTTGA 186
144 GTGGTGAATGCCAGCTGTCTCCCGTCATCTTGGGTGTCCAGGGTGAAGCCAGTGCCT 203
187 GCCTCATGTCTC-----TGTTCTTGGGAATCCATGGAGGGAGATGTGCTT 231
204 GTCATGTGGGGT---GGGACAGAGCCGACTCTTAACATGAGCCAGTGAATCATGGA 260
222 GTCTGTGTCAAGTCTGTGATGACACAGACTCCAGCTGAGGACGTTAATCATCTGA 291
261 GCTCTATCTTGGTGCCAAAGATCCAAAGACTTCACTTCAACCGCGGAGATGGGGCT 320
292 CTTGAGCGGAGAACAAAGACGAGACGAGGCTTCCGCTTATCCGTCAGACAGTGGCCC 351
321 CACCTTCAGCTTGAAGTGGCTGCTTACCCGCGGCTGTCTGTGCAAGCGTGCCTGAAGC 380
352 CACCAACAGTTTGAAGTGTGCGCGCTGCGCCGTTGTCTCTGCAACAGCATGGAGAC 411
381 CGATCAGCTGTGACATCAACCCAGCTTCCGAGATGGTGGC 423
412 TGACCAGCCCGTCAAGCTTCAACCAATATGCTTGAAGAGCGTGC 454

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RESULT 44

BM009048 955 bp mRNA linear EST 30-OCT-2001

LOCUS 603618892F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:5422918 5',

DEFINITION mRNA sequence.

ACCESSION BM009048

VERSION BM009048.1 GI:16523402

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE
1 (bases 1 to 955)
AUTHORS
TITLE
JOURNAL
COMMENT
Homidae; Homo.
1 (bases 1 to 955)
NIH-MGC <http://mgi.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1CM1881 row: h column: 23
High quality sequence stop: 792.

FEATURES
source
Location/Qualifiers
1..955
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="5422918"
/issue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 39"
/note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI;
Site: 2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGGCAGG(6). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-CDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies)."

ORIGIN
Query Match 23.2%; Score 108.6; DB 3; Length 955;
Best Local Similarity 58.6%; Pred. No. 7e-19;
Matches 236; Conservative 0; Mismatches 149; Indels 18; Gaps 2;

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QY 24 CTTCCGAATGAAGACTCGGCAATGAAGCTCTTATCTGCATATTAACCAAGCTTTAC 83
DB 92 CTTGCAATCTGGAGATGTTAACCAAGACCTTCTATCTGAGGAACAACCACTAGTTGC 151
QY 84 TGGAGGGCGCATGACGGAAGTCACTTAAGGTGAAGATCAGCTGTCCCAATG 143
DB 152 CGGATACCTTGCAAGGACCAATGTCAATTTAAGAAAGATGATGTGTACCACTTGA 211
QY 144 GTGGCTGATGTCAGGCTGTCCCGCTCATCTCGGCTGTCAGGGTGAAGCCAGTGCCT 203
DB 212 GCTCATGTCT-----TGTCTTGGAAATTCATGAGGGAAGATGTGCT 256
QY 204 GTCATGTGGGGTG---GGCAGAGCCGACTTAAACATAAGACCAATCATATGA 260
DB 257 GTCTGTGTCAAGTCTGTGATGAGACCAAGCTCCAGCTGAGGAGGAGTAAATCATCTGA 316
QY 261 GCTCATCTGTGTCGAAGGAATCCAAGAGCTTCACTTACCGCGGGAATGGGGCT 320
DB 317 CTTGAGCGAAGAACAGAAAGACAGACAGGCTTCCGCTTATCCGTCAGACAGTGGCC 376
QY 321 CACTTCAGACTTCAGAGTGGCTGCTTACCGGGCTGTCTCTGTGACAGGTCCTGAAGC 380
DB 377 CACCAACAGTTTGAAGTGTGCGCGCTGCGCGGTTGTCTCTGTGACAGCATGGAAGC 436
QY 381 CGATCAGCTGTGACATCAACCAAGCTTCCGGAATGTGGC 423
DB 437 TGACCAAGCCGTCAAGCTTCAACCAATATGCTGACGAAGGCGTC 479

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RESULT 45
AL540334 898 bp mRNA linear EST 24-MAR-2004
LOCUS AL540334 Homo sapiens PLACENTA Homo sapiens CDNA clone CS0DE001YA17
DEFINITION 5-PRIME, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AL540334
AL540334.3 GI:45715958
EST.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
1 (bases 1 to 898)
AUTHORS
TITLE
JOURNAL
COMMENT
Li, W.B., Gruber, C., Jesse, J. and Polyes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:30543383.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 1388.f
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?c=CS0DE001AA09qPlec=1388.f>.

FEATURES
source
Location/Qualifiers
1..898
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="CS0DE001YA17"
/issue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN
Query Match 23.1%; Score 108.2; DB 1; Length 898;
Best Local Similarity 58.3%; Pred. No. 9e-19;
Matches 225; Conservative 1; Mismatches 149; Indels 18; Gaps 2;

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QY 24 CTTCCGAATGAAGACTCGGCAATGAAGCTCTTATCTGCATATTAACCAAGCTTTAC 83
DB 123 CTTGCAATCTGGAGATGTTAACCAAGACCTTCTATCTGAGGAACAACCACTAGTTGC 182
QY 84 TGGAGGGCGCATGACGGAAGTCACTTAAGGTGAAGATCAGCTGTCCCAATG 143
DB 183 CGGATACCTTGCAAGGACCAATGTCAATTTAAGAAAGATGATGTGTACCACTTGA 242
QY 144 GTGGCTGATGTCAGGCTGTCCCGCTCATCTCGGCTGTCAGGGTGAAGCCAGTGCCT 203
DB 243 GCTCATGTCT-----TGTCTTGGAAATTCATGAGGGAAGATGTGCT 287
QY 204 GTCATGTGGGGTG---GGCAGAGCCGACTTAAACATAAGACCAATCATATGA 260
DB 288 GTCTGTGTCAAGTCTGTGATGAGACCAAGCTCCAGCTGAGGAGGAGTAAATCATCTGA 347
QY 261 GCTCATCTGTGTCGAAGGAATCCAAGAGCTTCACTTACCGCGGGAATGGGGCT 320
DB 348 CTTGAGCGAAGAACAGAAAGACAGACAGGCTTCCGCTTATCCGTCAGACAGTGGCC 407
QY 321 CACTTCAGACTTCAGAGTGGCTGCTTACCGGGCTGTCTCTGTGACAGGTCCTGAAGC 380
DB 408 CACCAACAGTTTGAAGTGTGCGCGCTGCGCGGTTGTCTCTGTGACAGCATGGAAGC 467
QY 381 CGATCAGCTGTGACATCAACCAAGCTTCCGGAATGTGGC 423
DB 468 TGACCAAGCCGTCAAGCTTCAACCAATATGCTGACGAAGGCGTC 510

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RESULT 46
AL554778      1069 bp      mRNA      linear      EST 30-MAR-2004
LOCUS
DEFINITION   AL554778 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1086YA15 5-PRIME, mRNA sequence.
ACCESSION
AL554778
VERSION
AL554778.3  GI:45859528
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 1069)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL
On Feb 15, 2001 this sequence version replaced gi:31276588.
COMMENT
Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1388.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0D1086YA08QPlc=1388.f.
FEATURES
source
1..1069
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1086YA15"
/rissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match      23.1%; Score 108.2; DB 1; Length 1069;
Best Local Similarity 58.3%; Pred. No. 9.3e-19;
Matches 225; Conservative 1; Mismatches 149; Indels 18; Gaps 2;
24 CTTCCGAATGAAAGACTCGCATTGAAGGCTTTATCTGCATTAATACAGGCTTACG 83
|||||
48 CTTGCAAAATCTGGAGATTTAACGAAAGACCTTCTATCTGAGAACACCACTAATTGC 107
|||||
84 TGGAGGGCTGATGATGAGGAGAGGATTTAAAGGTGAAGATCAGCGTGTCCCAATCG 143
|||||
108 CGGATACCTTGCAAGACCAAAATCTCAATTTAGAAAGAAAAGATGATGTGGTACCATTA 167
|||||
144 GTGGCTGATGATGCCAGCTGTCTCCCGTCATCTGGGTGTCAGGGTGAAGCCAGTGCT 203
|||||
168 GCCTCATGTCTC-----TGTTCTTGGGAATCCATGAGGAGGAGATGTGCTT 212
|||||
204 GTCATGTGGGGTNG---GGGAGAGGCGCACTTAACACTAGAGCCAGTGAACATCATGA 260
|||||
213 GTTCTGTGTCMAATCTGGTGATAGAACAGATCTCAGCTGGAGGCAAGTTAATCACTGA 272
|||||
261 GCTCTATCTTGTGCAAGATTCAGAGAGCTTCACTTCTACCGGCGGAGCAATGGAGCT 320
|||||
273 CTTGAGGAGAAACAGAAAGACAGACAGCGCTTCGCTTATCGCTCAAGACAGTGGCCC 332
|||||
321 CACCTTCAGCTTGAAGTGGCTGCTTACCCGGGCTGTTCTTGTCAGCGTGCCTGAAGC 380
|||||
333 CACCAACAGATTGATGCTGCTGCGCTGCGCGGTGGTTCCTGTGCAACAGATGAGAGC 392
|||||
381 CGATCAGCTGTGATGATCAACCAAGCTTCCCGAAGATGTGGC 423

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Db      393 TGACCAGCCCTCAGCTCAACCAATATGCTTGAGAGAGCGCTC 435
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RESULT 47
BM818991      403 bp      mRNA      linear      EST 06-MAR-2002
LOCUS
DEFINITION   BM818991 K-EST0086744 S20T665307 Homo sapiens cDNA clone S20T665307-5-D12
5'-mRNA sequence.
ACCESSION
BM818991
VERSION
BM818991.1  GI:19175404
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 403)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
JOURNAL
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kr.ibm.re.kr
Plate: 5 row: D column: 12
High quality sequence stop: 403.
FEATURES
source
1..403
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S20T665307-5-D12"
/sex="M"
/lab_host="Top10F"
/clone_lib="S20T665307"
/note="Organ: Stomach; Vector: pCNS; site: 1: EcoRI;
site: 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deacapped
with tabaco acid pyrophosphatase (TAP). The deacapped
cDNA was ligated with R4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
ORIGIN
Query Match      22.9%; Score 107; DB 3; Length 403;
Best Local Similarity 59.6%; Pred. No. 1.6e-18;
Matches 226; Conservative 0; Mismatches 135; Indels 18; Gaps 2;
48 GAAGTGCTTTATCTGCAATTAATACAGCTTCTAGCTGAGGCGCTGCAGAGGAAGT 107
|||||
21 GAAGACCTTCTATCTGAGGAAACAACTAGTGTGATTAATTGCAAGACCAATATGT 80
|||||
108 CATTAAGGTGAAGATCAGCGTGTCTCCCAATCGTGGCTGATGCCAGCTGTCTCCC 167
|||||
81 CAATTTAGAAAGAAATGATGTGTATCCATTTGAGCCTCATGCTC----- 127
|||||
168 CGTATCTGTGGTGTCCAGGTGAAGCCAGTGCCTGTCAATGTG---GGTGGGACAGA 224
|||||

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Db 128 --TGTTCTGGGAATCATGAGGAGAAATGTCCTGCTGTGCAAGTGTGTATGA 185
QY 225 GCGCACTTAACAGTGAAGCAGTGAACATCATGAGCTTATCTGTGTGCCAAGAAATC 284
Db 186 GACCAACTTCAGCTGAGGACATTAATCACTGACTGAGGAGAAACAGAAAGACAGA 245
QY 285 CAAGAGCTTACCTTCTACCGGCGGAGACATGAGGCTCACCTCCAGCTTCGAGTGGCTGC 344
Db 246 CAAGGCTTCGCTTATCCGCTCAGACAGCGGCCACACAGTTTGAAGTCTGCGCG 305
QY 345 CTACCCGGGCTGTTCTCTGTGCACGGTCTGAAGCCGATCAGCTGTGACACTCACCA 404
Db 306 CTGCCCCGGTGGTCTCTGTGCACAGGATGAAAGCTGACAGCCGCTGACCTCACAA 365
QY 405 GCTTCCCGAAGATGTGGC 423
Db 366 TATGCTTGACGAAGCGCTC 384

RESULT 48
LOCUS BG288796 640 bp mRNA linear EST 21-FEB-2001
DEFINITION BG288796 602388126F1 NIH_MGC_93 Homo sapiens cDNA IMAGE:4516927 5',
mRNA sequence.
ACCESSION BG288796
VERSION BG288796.1 GI:13043994
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 640)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Place: LLM10409 row: c column: 08
High quality sequence stop: 635.
Location/Qualifiers
1. 640
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/db_xref="taxon:9606"
/clone="IMAGE:4516927"
/tissue_type="transfected cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_93"
/note="Organ: bladder; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."

FEATURES
source
ORIGIN
Query Match 22.9%; Score 107; DB 2; Length 640;
Best Local Similarity 59.6%; Pred. No. 1.8e-18;
Matches 226; Conservative 0; Mismatches 135; Indels 18; Gaps 2;

QY 48 GAAGGCTTATTCGATATTAACAGCTTCTAGCTGAGGCGTGCATGAGGAGAGT 107
Db 2 GAAGACCTTCTATCTGAGAACACCACTAGTGTGATCTTGCAAGACCAATAT 61
QY 108 CATTAAGGTGAAGATCAGCGGTGCTCCCAATCGGTGCTGATGCGAGCTGTCCC 167

Db 62 CAATTAGAAAAGATAGATGTGTGATCCATTGAGCCTCATGCTC----- 108
QY 168 CGTATCTCTGGGTGTCCAGGATGAGACCAAGTGCCTGTCAATGTG---GCTGGGACAGA 224
Db 109 --TGTTCTGGGAATCATGAGGAGAAATGTCCTGCTGTGCAAGTGTGTATGA 186
QY 225 GCGCACTTAACAGTGAAGCAGTGAACATCATGAGCTTATCTGTGTGCCAAGAAATC 284
Db 167 GACCAACTTCAGCTGAGGACATTAATCACTGACTGAGGAGAAACAGAAAGACAGA 226
QY 285 CAAGAGCTTACCTTCTACCGGCGGAGACATGAGGCTCACCTCCAGCTTCGAGTGGCTGC 344
Db 227 CAAGGCTTCGCTTATCCGCTCAGACAGCGGCCACACAGTTTGAAGTCTGCGCG 286
QY 345 CTACCCGGGCTGTTCTCTGTGCACGGTCTGAAGCCGATCAGCTGTGACACTCACCA 404
Db 287 CTGCCCCGGTGGTCTCTGTGCACAGGATGAAAGCTGACAGCCGCTGACCTCACAA 346
QY 405 GCTTCCCGAAGATGTGGC 423
Db 347 TATGCTTGACGAAGCGCTC 365

RESULT 49
LOCUS BG987216 120 bp mRNA linear EST 13-JUN-2001
DEFINITION BG987216 MR2-HT1161-050101-004-cl2_1 HT1161 Homo sapiens cDNA, mRNA
sequence.
ACCESSION BG987216
VERSION BG987216.1 GI:14391286
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 120)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Coستا, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the RAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR2&cl2=MR2-HT1161-050101-004-cl2> let3=2001-01-05&cl=1)
Seq primer: puc 18 forward
High quality sequence stop: 84.
Location/Qualifiers
1. 120
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT1161"
/note="Organ: head_neck; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of

FEATURES
source

ORIGIN

tissue mRNA and cDNA amplification were performed under low stringency conditions."

Query Match 22.2%; Score 103.8; DB 2; Length 120;
Best Local Similarity 96.7%; Pred. No. 9.9e-18;
Matches 116; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 105 GGTCTTAAAGGTGAAGATCAGCGTGTCCCAATCGTGGCTGATG-CCAGCCTGT 163
DB 1 GGTCTTAAAGGTGAAGATCAGCGTGTCCCAATCGGCGGCTGATGCGCAGNCTGT 60
QY 164 CCCCCGTATCTGGGTGTCCAGGCTGAAGCCAGTGCCTGTCATGTGGGGTGGCAGG 223
DB 61 CCCCCGTATCTGGGTGTCCAGGCTGAAGCCAGTGCCTGTCATGTGGGGTGGCAGG 120

RESULT 50
DQ043278

LOCUS DQ043278 435 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens IL1F10 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

ACCESSION DQ043278
VERSION DQ043278.1 GI:66894493

KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1 (bases 1 to 435)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civeello,D.,
White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
(et) Plos Biol. 3 (6), E170 (2005)

JOURNAL 15869325
PUBMED 2 (bases 1 to 435)
REFERENCE Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B.,
AUTHORS Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civeello,D.,
White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission

TITLE Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
JOURNAL Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.

FEATURES
source 1..435
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/locus_tag="HC10058"

ORIGIN

Query Match 22.2%; Score 103.8; DB 11; Length 435;
Best Local Similarity 62.2%; Pred. No. 1.3e-17;
Matches 181; Conservative 0; Mismatches 107; Indels 3; Gaps 1;

QY 118 GAAGATCAGCGTGTCCCAATCGTGGCTGATGCCAGCTGTCCCGCTCATCTG 177
DB 94 GAGAGATCTGCATCTCTTAACAAGGCTTGCCGCCACCAAGGTCCCATTTTCCTG 153
QY 178 GGATTCAGGTTGAAGCCAGTGCCTGTCAATGNGGGTG---GGGAGAGAGCCGACTTA 234
DB 154 GGGATCAGAGAGAGAGCCGCTGCTGTCATGTGTGAAGACAGAGAGGGGCTTCCTTA 213
QY 235 ACAGTAGAGCACTGAACATCATGAGCTCTATCTTGTCGCAAGGATCCAGAGCTTC 294

DB 214 CAGCTGAGAGATGTGAACATTGAGGAAGTGTGTAAGAGGCCACAGCGCTTC 273
QY 295 ACCTTTACCGGCGGGAGCATGGGGCTCACCTCCAGCTTCGAGTGGCTGCCTAACCGGGC 354
DB 274 ACCTTTCCAGAGACAGCTCAGGCTCCGCTTCAGGCTTGAGGCTGCTGGCTGGC 333
QY 355 TGGTTCCTGTGACAGTGCCTGAAGCCGATGAGCTGTCAAGCTCACCCAG 405
DB 334 TGGTTCCTGTGTGGCCCGGAGAGCCCGCAGAGCCAGTCAAGCTTACCAAG 384

Search completed: January 27, 2006, 21:51:48
Job time : 3090 secs